PDB annotation		TRANSCRIPTION REGULATION GENE REGULATING PROTEIN, TRANSCRIPTION REGULATION		COMPLEX (DNA-BINDING PROTEIN/DNA) HD; HOMEODOMAIN, COMPLEX (DNA- BINDING PROTEIN/DNA)			PROTEIN/DNA HOMEODOMAIN, DNA, COMPLEX, DNA-BINDING PROTEIN, PROTEIN/DNA	TRANSCRIPTION/DNA ULTRABITHORAX; PBX PROTEIN; DNA BINDING, HOMEODOMAIN, HOMEOTIC PROTEINS, DEVELOPMENT, 2 SPECIFICITY	COMPLEX (DNA-BINDING PROTEIN/DNA) DNA-BINDING
Coumpound	WITH CYS 39 ISAN 3 REPLACED BY SER AND RESIDUES 1-6 DELETED (C39S,DEL 1-6) ISAN 4 (NMR, 20 STRUCTURES) ISAN 5	PHAGE 434 CRO PROTEIN; CHAIN: NULL;	GENE REGULATING PROTEIN CRO PROTEIN 2CRO 4	ANTENNAPEDIA PROTEIN; CHAIN: A, B; DNA; CHAIN: C, D, E, F;		DNA-BINDING PROTEIN ANTENNAPEDIA PROTEIN (HOMEODOMAIN) MUTANT WITH CYS 39 1AHD 3 REPLACED BY SER (C39S) COMPLEX WITH DNA (NMR, 1AHD 4 16 STRUCTURES) 1AHD 5	HOMEOBOX PROTEIN HOX-B1; CHAIN: A; PBX1; CHAIN: B; DNA CHAIN: D; DNA CHAIN: E;	ULTRABITHORAX HOMEOTIC PROTEIN IV; CHAIN: A; HOMEOBOX PROTEIN EXTRADENTICLE; CHAIN: B; DNA (5'- CHAIN: C; DNA (5'- CHAIN: D;	PAIRED PROTEIN; CHAIN: A, B, C; DNA; CHAIN: D, E, F
SEQFOL D score	·								
PMF score		0.17	0.29	0.04		0.18	0.07	0.28	0.92
Verify score		-0.16	-0.59	-0.27		-0.46	-0.02	-0.31	-0.04
Psi Blast		0.0003	0.0003	3.2e-26		1.6e-28	1.5e-24	8e-24	1.6e-23
END		205	205	341	***	347	343	340	341
STAR T AA		173	173	271		267	271	27.1	266
CHAI N ID	•			٧	e de la composition della comp	A	4	∢	Ą
PDB ID		1zug	2cro	9ant		lahd	1672	1581	161
SEQ ID NO:	·	1733	1733	1733		1734	1734	1734	1734

		·	· ·					,																
PDB annotation	PROTEIN, DNA, PAIRED BOX, TRANSCRIPTION 2 REGULATION	COMPLEX (DNA-BINDING PROTEIN/DNA) DNA-BINDING PROTEIN, DNA, PAIRED BOX, TRANSCRIPTION 2 REGIT ATION																	TRANSCRIPTION REGULATION	GENE REGULATING PROTEIN,	TRANSCRIPTION REGULATION		COMPLEY (PNIA PRIDATE	PROTEIN/DNA) HD:
Coumpound		PAIRED PROTEIN; CHAIN: A, B, C; DNA; CHAIN: D, E, F	TRANSCRIPTION REGULATION TRANSCRIPTION FACTOR LFB1 (HOMEODOMAIN) 11.FB 3	GENE REGULATING PROTEIN	REPRESSOR PROTEIN FROM BACTERIOPHAGE 434 (DNA-	BINDING 1PRA 3 DOMAIN,	RESIDUES 1-69) (NMR, 20 STRUCTURES) IPRA 4	GENE REGULATING PROTEIN	REPRESSOR (AMINO-	TERMINAL DOMAIN) (R1-69)	DNA-BINDING PROTEIN	ANTENNAPEDIA PROTEIN	(HOMEODOMAIN) MUTANT	WITH CYS 39 ISAN 3	REPLACED BY SER AND	RESIDUES 1-6 DELETED	(C39S,DEL 1-6) 1SAN 4 (NMR, 20	STRUCTURES) 1SAN 5	PHAGE 434 CRO PROTEIN;	CHAIN: NULL;		GENE REGULATING PROTEIN	ANTENNA DEDIA DE OTENI	CHAIN: A, B; DNA; CHAIN; C,
SEQFOL D score																								
PMF score		1.00	0.99	0.51				0.78			0.19	}							0.17			0.29	000	† 2.0
Verify score		0.38	0.61	0.08				0.15			0.09	}							-0.16			-0.59	-0.27	77.0
Psi Blast		8e-22	6e-24	0.00015				0.0003			6.4e-26								0.0003			0.0003	86-26	27-20
END		339	336	205				205			347								205			205	341	ξ.
STAR T AA		267	271	173		-		173			273								173	- -		173	271	
CHAI N ID		æ																				_	A	
PDB ID		149	11fb	Brdl				1169			1 san								lzug			2cro	Qant	
SEQ NO:		1734	1734	1734				1734			1734								1734			1734	1734	

	PDB annotation	HOMEODOMAIN, COMPLEX (DNA- BINDING PROTEIN/DNA)	MUSCLE PROTEIN CTNC; CARDIAC, MUSCLE PROTEIN, REGULATORY, CALCIUM BINDING	MUSCLE PROTEIN CTNC; CARDIAC, MUSCLE PROTEIN, REGULATORY, CALCIUM BINDING	MUSCLE PROTEIN CTNC; CARDIAC, MUSCLE PROTEIN, REGULATORY, CALCIUM BINDING	CALCIUM-BINDING PROTEIN CALMODULIN CERIUM TRIC- DOMAIN, RESIDUES 1 - 75; CERIUM- LOADED, CALCIUM-BINDING PROTEIN	CALCIUM-BINDING CNTNC; CALCIUM-BINDING, REGULATION, TROPONIN C, CARDIAC MUSCLE 2 CONTRACTION	HYDROLASE CALCINEURIN; HYDROLASE, PHOSPHATASE, IMMUNOSUPPRESSION	MUSCLE CONTRACTION MUSCLE CONTRACTION, CALCIUM- ACTIVATED, TROPONIN, E-F HAND 2 CALCIUM-BINDING PROTEIN	CALCIUM-BINDING PROTEIN SNTNC; CALCIUM-BINDING, REGULATION, TROPONIN C, SKELETAL MUSCLE CONTRACTION	MUSCLE PROTEIN MDE; MUSCLE
	Coumpound	D, E, F;	TROPONIN C; CHAIN: NULL;	TROPONIN C; CHAIN: NULL;	TROPONIN C; CHAIN: NULL;	CALMODULIN; CHAIN: NULL;	CARDIAC N-TROPONIN C; CHAIN: NULL;	SERNE/THREONINE PHOSPHATASE 2B; CHAIN: A, B;	TROPONIN C; CHAIN: A, B;	N-TROPONIN C; CHAIN: NULL;	MYOSIN; CHAIN: A, B, C, D, E,
	SEQFOL D score		:	82.97		75.36	61.36	·	70.90	71.63	57.30
	PMF		0.06		0.70			-0.01			
มหังการกับพ.ษ.การการครั้งใ	Verify		-0.11		0.17			0.08			
1	Psi Blast		4.8e-30	1.4e-38	1.4e-38	1.16-29	6.4e-23	3.2e-20	3.2e-26	8e-27	4.8e-34
	END		101	170	169	104	109	101	106	109	170
	STAR T AA			23	25	30	72	_	26	50	33
	CHAI N ID					·		В	∀		В
	EDB CI		1aj4	laj4	1aj4	1ak8	lap4	laui	Iavs	1blg	1br1
	SEQ NO:		1738	1738	1738	1738	1738	1738	1738	1738	1738

PDB annotation	PROTEIN	CALCIUM BINDING CALCIUM BINDING		· · · · · · · · · · · · · · · · · · ·		· · · · · · · · · · · · · · · · · · ·			-										0									CALCIUM-BINDING PROTEIN CALMODULIN APO TR2C-DOMAIN;	STRUCTURAL PROTEIN HELIX-	
Coumpound	F, G, H;	CALCIUM-BINDING PROTEIN; CHAIN: NULL;	CALCIUM-BINDING PROTEIN	WITH CALMODULIN-BINDING	DOMAIN OF 1CDM 3	CALMODULIN-DEPENDENT	PROTEIN KINASE II ICDM 4	CALCIUM-BINDING PROTEIN	CALIMODULIN COMPLEXED	WITH CALMODULIN-BINDING	DOMAIN OF ICOM 3	CALMODULIN-DEPENDENT	PROTEIN KINASE II 1CDM 4	CALCIUM-BINDING PROTEIN	CALMODULIN COMPLEXED	WITH CALMODULIN-BINDING	DOMAIN OF 1CDM 3	CALMODULIN-DEPENDENT	PROTEIN KINASE II 1CDM 4	CALCIUM-BINDING PROTEIN	CALMODULIN (VERTEBRATE)	ICLL 3	CALCIUM-BINDING PROTEIN	CALMUDULIN (VERTEBRATE)	Out on a familiary and an output	CALCIUM-BINDING PROTEIN CALMODULIN (VERTEBRATE)	ICLL 3	CALMODULIN (VERTEBRATE); 1CMF 6 CHAIN: NULL; 1CMF 7	CARDIAC TROPONIN C;	
SEQFOL D score		50.72						85.63	,											,		-		}	60	28.82		68.52		
PIMF score			0.82											0.92						0.40			0.81						0.28	
Verify score			0.01											0.08						-0.09			-0.02						0.00	
Psi Blast		3.2e-11	8e-35					1.4e-47						1.4e-47						3.2e-35			9.6e-53		0.5.5.0	7.0e-53		7.5e-23	4.8e-29	
END		103	102	-			1	158						169						102		i	169		0,0	2		401	101	
STAR T AA		2	1					33						33									33		23	55		33	-	!
CHAI N ID		***	Ą					∢						∢						•	•		• =	7					Ą	
PDB ID		1bu3	lodm					<u> </u>						lodin						leli			101		110	101		lcmf	1dtl	
SEQ ID NO:		1738	1738					1738	s					1738	*****			••••		1738			1738		1720	1738		1738	1738	

PDB annotation	CONTRACTION, CALCIUM- BINDING, TROPONIN, E-F HAND, 2 OPEN CONFORMATION REGULATORY DOMAIN, CALCIUM- REGULATED 3 MUSCLE CONTRA ACTION				ļ	P ₃	£ d.	JF TRC	4IN E)	CALMODULIN, CALCIUM BINDING, HELIX-LOOP-HELIX, SIGNALLING, 2 COMPLEX(CALCIUM-BINDING	CHCITTATE/VIETCAG
Coumpound		TROPONIN C; ITNX 4 CHAIN: NULL: ITNX 5	TROPONIN C; 1TNX 4 CHAIN: NULL; 1TNX 5	TROPONIN C; 1TNX 4 CHAIN: NULL; 1TNX 5	CONTRACTILE SYSTEM PROTEIN TROPONIN C 1TOP 3	CONTRACTILE SYSTEM PROTEIN TROPONIN C 1TOP 3	CONTRACTILE SYSTEM PROTEIN TROPONIN C 170P 3	CALCIUM BINDING PROTEIN CALMODULIN (/TR=2=C\$ FRAGMENT COMPRISING RESIDUES 78 - 148 ITRC 3 OF THE INTACT MOLECULE) ITRC	MUSCLE PROTEIN TROPONIN C (TRIC FRAGMENT) (APO FORM) (NMR, 1 STRUCTURE) 1TRF 3	CALMODULIN; CHAIN: A; RS20; CHAIN: B;	
SEQFOL D score			84.53			96.98		62.97	66.58		
PMF		0.41		0.94	0.30		1.00			0.36	
Verify		-0.26		0.17	-0.20		0.13			-0.06	
Psi Blast		9.6e-34	1.6e-38	1.6e-38	3.2e-32	4.8e-42	4.8e-42	.8e-22	3.2e-26	9.6e-36	-
END		101	169	169	101	169	169	103	106	104	
STAR T AA			24	33	1	20	33	36	31	-	
CHAI N ID	•							∢		A	
PDB CI		1tmx	1 tmx	ltnx	Itop	1top	Itop	ी ज्	1tf	lvrk	
SEQ No.		1738	1738	1738	1738	1738	1738	1738	1738	1738	

PDB annotation	COMPLEX(CALCIUM-BINDING PROTEIN/PEPTIDE)	CALMODULIN, CALCIUM BINDING, HELIX-LOOP-HELIX, SIGNALLING, 2 COMPLEX(CALCIUM-BINDING PROTEIN/PEPTIDE)	MUSCLE PROTEIN MYOSIN, CALCIUM BINDING PROTEIN, MUSCLE PROTEIN	MUSCLE PROTEIN MYOSIN, CALCIUM BINDING PROTEIN, MUSCLE PROTEIN	CALCIUM-BINDING PROTEIN CTNC; CARDIAC, MUSCLE, REGULATORY, CALCIUM-BINDING PROTEIN			TRANSFERASE ATP:AMP- PHOSPHOTRANSFERASE, TRANSFERASE		
Coumpound		CALMODULIN; CHAIN: A; RS20; CHAIN: B;	SCALLOP MYOSIN; CHAIN: A, B, C;	SCALLOP MYOSIN; CHAIN: A, B, C;	TROPONIN C; CHAIN: NULL;	CALCIUM BINDING CALCIUM- BINDING PARVALBUMIN (\$P*I=4.25) 4CPV 3	TRANSFERASE URIDYLATE KINASE (B.C.2.7.4) COMPLEXED WITH ADP AND AMP 1UKZ 3	ADENYLATE KINASE; CHAIN: A, B;	TRANSFERASE(PHOSPHOTRA NSFERASE) ADENYLATE KINASE (E.C.2.7.4.3) 3ADK 4	TRANSFERASE URIDYLATE KINASE (E.C.2.7.4) COMPLEXED WITH ADP AND AMP 111K7 3
SEQFOL D score			64.97	54.16	52.43	51.70				
PMF score		0.95					0.07	0.13	0.16	0.07
Verify score		0,15					-0.05	-0.17	-0.25	-0.05
Psi Blast		1.1e-51	7.5e-26	1.18-25	8e-10	1.3e-11	0.0006	0.0001	0.0075	0.0006
END AA		169	170	171	104	103			495	463
STAR T AA		33	33	33	31	9	362	362	362	362
CHAI N ID		Ą	В	၁				∢		
PDB ID		lvrk	1wdc	lwdc	3ctn	4cpv	lukz	1zak	3adk	lukz
SEQ NO:		1738	1738	1738	1738	1738	1745	1745	1745	1746

All a second described by

PDB annotation	TRANSFERASE ATP:AMP. PHOSPHOTRANSFERASE, TRANSFERASE		TRANSFERASE BRUTON'S	AGAMMAGLOBULINEMIA TYROSINE KINASE, BTK:	TRANSFERASE, PH DOMAIN, BTK	MOTIF, ZINC BINDING, X-LINKED 2	TYROSINE-PROTEIN KINASE	SIGNALING PROTEIN DAPP1, PHISH,	BAM32; PLECKSTRIN, 3-	THOSPHOINOSITIDES, INUSTITUTE OF STATES	TRANSPICTION PROTEIN	ADAPTOR PROTEIN	SIGNALING PROTEIN DAPP1, PHISH,	BAM32; PLECKSTRIN, 3-	PHOSPHOINOSITIDES, INOSITOL	TETRAKISPHOSPHATE 2 SIGNAL	IRANSDUCTION PROTEIN, ADAPTOR PROTEIN	SIGNALING PROTEIN ARF1	GUANINE NUCLEOTIDE EXCHANGE FACTOR AND PH DOMAIN	HYDROLASE METALLO-BETA-	LACTAMASE, ANTIBIOTIC PESISTANCE DEFICE EAD 3 ZINC	HYDROLASE
Coumpound	ADENYLATE KINASE; CHAIN: A, B;	TRANSFERASE(PHOSPHOTRA NSFERASE) ADENYLATE KINASE (E.C.2.7.4.3) 3ADK 4	BRUTON'S TYROSINE KINASE;	CHAIN: A, B;				DUAL ADAPTOR OF	CHOSPHOTYROSINE AND 3-	CHAIN: A;			DUAL ADAPTOR OF	PHOSPHOTYROSINE AND 3-	CHAIN: A;			GRP1; CHAIN: A;		PENICILLINASE; CHAIN: A;		
SEQFOL D score				:		1 s.f																
PMF score	0.13	0.16	0.04					0.83				i	0.99					0.75		-0.14		
Verify	-0.17	-0.25	-0.50		`			0.14					0.25					-0.02		80.0		
Psi Blast	0.0001	0.0075	90-99					3e-15					3e-16			_		7.5e-12		1.6e-14		
END AA	587	495	142					142					142					142		178		
STAR T AA	362	362	53					55					48		-			52		3		
CHAI N ID	∢		Ą		,			¥					¥					¥		¥	•	
PDB ID	1zak	3adk	16tk				-	Ifao					1fb8	-				Ifgy		lmsi		
SEQ TO	1746	1746	1749					1749					1749					1749		1750		

PDB annotation	ASE HYDROLASE HYDROLASE, BETA- LACTAMASE, ANTIBIOTIC, METALLOENZYME	OXIDOREDUCTASE	METALLOPROTEIN, FE(II)	OXIDOREDUCTASE OXIDOREDUCTASE,	METALLOPROTEIN, FE(II) COMPLEX, CATECHOL	-	ZINC PHOSPHOLIPASE C,	GANGRENE DETERMINANT, C2	DOMAIN, CA 2 AND MEMBRANE BINDING. HYDROLASE			TRIACYLGLYCEROL LIPASE	CONTRACTOR	(HYDROLASE/COFACTOR), LIPID DEGRADATION						METALLOPROTEIN, FATTY ACIDS		LIPOXYGENASE, METALLOPROTEIN RATTY ACIDS	
Coumpound	METALLO BETA-LACTAMASE II; CHAIN: A, B;	LIPOXYGENASE-3; CHAIN:	,	LIPOXYGENASE-3; CHAIN: NULL;		ALPHA-TOXIN; CHAIN: NULL;				TRIACYLGLYCEROL ACYL-	HYDROLASE; CHAIN: A, C;	COLIPASE; CHAIN: B, D		-	15-LIPOXYGENASE; CHAIN:	NULL;	15-LIPOXYGENASE; CHAIN:	NULL;	LIPOXYGENASE-1; CHAIN:	NOLL;	LIPOXYGENASE-1; CHAIN:	NULL;	
SEQFOL D score		253.58															482.93		231.83				
PMF score	-0.05			1.00		0.04				0.45					1.00						1.00		
Verify score	0.18			0.36		-0.01				0.46					0.41						0.18		
Psi Blast	1.6e-14	0		0		1.6e-20				0.0045					0		0		0	,	0		
END	170	711		711		111				66					711		711		711		711		
STAR T AA	E	ī		35		7				4					2		7		-		46		
CHAI N ID	∢									Ą				•						_			
PDB ID	2bc2	15yt		1634		[ca]				1eth					llox		1 ox		1yge		1yge		
SEQ ID No.	1750	1751		1751		1751				1751					1,221		1751		1751	• 10	1751		

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PDB annotation	SIGNALING PROTEIN GTP-BINDING PROTEIN RHOA, GTPASE RHOA; RHO GDI I; RHO GTPASE, G- PROTEIN, SIGNALING PROTEIN	SIGNALING PROTEIN GTP-BINDING PROTEIN RHOA, GTPASE RHOA; RHO GDI I; RHO GTPASE, G- PROTEIN, SIGNALING PROTEIN	CELL CYCLE CDC42; RHO GDI 1; GTP-BINDING PROTESSPECTZ, RHOGDI, X-RAY	CELL CYCLE CDC42; RHO GDI 1; GTP-BINDING PROTEIN, CDC42, RHOGDI, X-RAY		,	PROTEIN/DNA HOMEODOMAIN, DNA, COMPLEX, DNA-BINDING PROTEIN, PROTEIN/DNA
Coumpound	TRANSFORMING PROTEIN RHOA; CHAIN: A, C; RHO GDP DISSOCIATION INHIBITOR ALPHA; CHAIN: E, F;	TRANSFORMING PROTEIN RHOA; CHAIN: A, C; RHO GDP DISSOCIATION INHIBITOR ALPHA; CHAIN: E, F;	GTP-BINDING PROTEIN; CHAIN: A; GDP-DISSOCIATION INHIBITOR 1; CHAIN: B;	GTP-BINDING PROTEIN; CHAIN: A; GDP-DISSOCIATION INHIBITOR 1; CHAIN: B;	DNA-BINDING PROTEIN ANTENNAPEDIA PROTEIN (HOMEODOMAIN) MUTANT WITH CYS 39 1AHD 3 REPLACED BY SER (C39S) COMPLEX WITH DNA (NMR, 1AHD 4 16 STRUCTURES) 1AHD 5	DNA-BINDING PROTEIN ANTENNAPEDIA PROTEIN (HOMEODOMAIN) MUTANT WITH CYS 39 1AHD 3 REPLACED BY SER (C39S) COMPLEX WITH DNA (NMR, 1AHD 4 16 STRUCTURES) 1AHD 5	HOMEOBOX PROTEIN HOX-BI; CHAIN: A; PBXI; CHAIN: B; DNA CHAIN: D; DNA CHAIN: E;
SEQFOL D score					 70.63	·	
PMF	1.00	1.00	1.00	1.00		0.90	0.98
Verify	0:50	0.33	0.48	0.48	·	-0.12	-0.15
Psi Blast	4.5e-66	9.6e-70	6e-76	1.6e-78	6.4e-36	6.4e-36	3e-31
END AA	162	177	162	180	98	82	81
STAR T AA	24	24	ις.	رم ا		20	21
CHAI N ID	trj	<u>. </u>	а	Ф	۵,	ъ	4
PDB ID	0001	1000	ldoa	1doa	lahd	lahd	1672
SEQ ID NO:	1753	1753	1753	1753	 1757	1757	1757

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PDB annotation	PROTEIN/DNA HOMEODOMAIN, DNA, COMPLEX, DNA-BINDING PROTEIN, PROTEIN/DNA	PROTEIN/DNA HOMEODOMAIN, DNA, COMPLEX, DNA-BINDING PROTEIN, PROTEIN/DNA	TRANSCRIPTION/DNA ULTRABITHORAX; PBX PROTEIN; DNA BINDING, HOMEODOMAIN, HOMEOTIC PROTEINS, DEVELOPMENT, 2 SPECIFICITY	TRANSCRIPTION/DNA ULTRABITHORAX; PBX PROTEIN; DNA BINDING, HOMEODOMAIN, HOMEOTIC PROTEINS, DEVELOPMENT, 2 SPECIFICITY				
Coumpound	HOMEOBOX PROTEIN HOX-BI; CHAIN: A; PBXI; CHAIN: B; DNA CHAIN: D: DNA CHAIN: E:	HOMEOBOX PROTEIN HOX-B1; CHAIN: A; PBX1; CHAIN: B; DNA CHAIN: D; DNA CHAIN: E;	ULTRABITHORAX HOMEOTIC PROTEIN IV; CHAIN: A; HOMEOBOX PROTEIN EXTRADENTICLE; CHAIN: B; DNA (5'- CHAIN: C; DNA (5'- CHAIN: D;	ULTRABITHORAX HOMEOTIC PROTEIN IV; CHAIN: A; HOMEOBOX PROTEIN EXTRADENTICLE; CHAIN: B; DNA (5'- CHAIN: C; DNA (5'- CHAIN: D;	DNA-BINDING FUSHI TARAZU PROTEIN (HOMEODOMAIN) (NMR, 20 STRUCTURES) IFTZ 3	DNA-BINDING FUSHI TARAZU PROTEIN (HOMEODOMAIN) (NMR, 20 STRUCTURES) IFTZ 3	(POU DOMAIN) 10CT 3	DNA-BINDING PROTEIN ANTENNAPEDIA PROTEIN (HOMEODOMAIN) MUTANT WITH CYS 39 ISAN 3 REPLACED BY SER AND RESIDUES 1-6 DELETED (C39S,DEL 1-6) ISAN 5 STRUCTURES) ISAN 5
SEQFOL D score		64.24	64.34		66.44			65.69
PMF	0.99			0.82		0.81	0.23	
Verify score	0.19			-0.14		-0.01	-0.70	
Psi Blast	3.2e-28	3e-31	6.4e-31	6.4e-31	4.8e-32	4.8e-32	3e-31	1.6e-33
END AA	81	81	77	78	98	58	64	98
STAR T AA	24	6	50	7	18	61	p-rel	2.5
CHAI N ID	A	A	∢	¥			ပ	
PDB	1672	1672	1b8i	158i	यमु १	lfiz	loct	lsan
SEQ ID	NO: 1757	1757	1757	1757	1757	1757	. 1757	1757

PDB annotation		COMPLEX (DNA-BINDING PROTEIN/DNA) HD; HOMEODOMAIN, COMPLEX (DNA- BINDING PROTEIN/DNA)	COMPLEX (DNA-BINDING PROTEIN/DNA) HD; HOMEODOMAIN, COMPLEX (DNA-BINDING PROTEIN/DNA)	LIPOCALIN LIPOCALIN, OLFACTION	SUGAR BINDING PROTEIN NGAL; NEUTROPHIL, NGAL, LIPOCALIN	ALLERGEN LIPOCALIN, BETA BARREL			ODORANT-BINDING PROTEIN OBPOLFACTION, NOSE, TRANSPORT, LIPOCALIN, ODORANT-BINDING 2
Coumpound	DNA-BINDING PROTEIN ANTENNAPEDIA PROTEIN (HOMEODOMAIN) MUTANT WITH CYS 39 1SAN 3 REPLACED BY SER AND RESIDUES 1-6 DELETED (C39S,DEL 1-6) 1SAN 5 STRUCTURES) 1SAN 5	ANTENNAPEDIA PROTEIN; CHAIN: A, B; DNA; CHAIN: C, D, E, F;	ANTENNAPEDIA PROTEIN; CHAIN: A, B; DNA; CHAIN: C, D, E, F;	ODORANT BINDING PROTEIN; CHAIN: A, B;	HUMAN NEUTROPHIL GELATINASE; CHAIN: A, B;	ALLERGEN EQU C 1; CHAIN: A;	PHEROMONE-BINDING MAJOR URINARY PROTEIN COMPLEX WITH 2-(SEC-BUTYL) IMUP 3 THIAZOLINE IMUP 4	PHEROMONE-BINDING MAJOR URINARY PROTEIN COMPLEX WITH 2-(SEC-BUTYL) IMUP 3 THIAZOLINE IMUP 4	ODORANT-BINDING PROTEIN; CHAIN: A, B;
SEQFOL D score			68.97					64.35	
PMF score	0.98	1.00		0.86	1.00	0.95	00'1	;	-0.02
Verify score	-0.17	-0.13		0.63	99'0	06:0	0.78		0.19
Psi Blast	1.6e-33	1.6e-33	1.6e-33	3e-35	4.5e-47	1.4e-38	6e-3 <i>7</i>	6e-37	9e-36
END	\$8	79	7.9	691	169	169	168	168	172
STAR T AA	26	24	24	38	20	30	25	25	30
CHAI N ID		Ą	Y	Æ	¥	A			Ą
PDB ID	lsan	9ant	9ant	1a3y	1dfv	lew3	lmup	dnwj	lobp
SEQ ID NO:	1757	1757	<i>LSL</i> 1	1758	1758	1758	1758	1758	1758

SEPO PDB CHAI STAR END Psi Blast Verify PMF SEQPOL Coumpound PDB annotation PBB annotation PBB annotation PBB annotation PBC 175								,						·					
PDB CHAI STAR END Psi Blast Verify PMF SEQFOL		PDB annotation	PROTEIN SUGAR BINDING PROTEIN NGAL; NEUTROPHIL LIPOCALIN, SIGNAL PROTEIN, GLYCOPROTEIN		LIPID BINDING PROTEIN A2U- GLOBULIN, LIPID BINDING PROTEIN	LIPID BINDING PROTEIN A2U- GLOBULIN, LIPID BINDING PROTEIN	LIPID BINDING PROTEIN A2U- GLOBULIN, LIPID BINDING PROTEIN		COMPLEX (VIRAL CAPSID/IMMUNOGLOBULIN) HIV-1	CA, HIV CA, HIV P24, P24; FAB, FAB	COMPLEX (VIRAL	CAPSID/IMMUNOGLOBULIN), HIV, CAPSID PROTEIN, 2 P24	COMPLEX (MHC/VIRAL PEPTIDE/RECEPTOR) HLA-A2	HEAVY CHAIN; CHEST MHC, T.	COMPLEX (MHC/VIRA)	PEPTIDE/RECEPTOR	IMMUNOGLOBULIN HUMAN FAB,	AFFINITY, CRYSTAL 2 PACKING	MOTIF, FROM AND WHING
PDB CHAI STAR END Psi Blast Verify PMF		Соитроина	NEUTROPHIL GELATINASE; CHẠIN: A;	RETINOL TRANSPORT RETINOL BINDING PROTEIN IRBP 3	ALPHA-2U-GLOBULIN; CHAIN: A, B, C, D	ALPHA-2U-GLOBULIN; CHAIN: A, B, C, D	ALPHA-2U-GLOBULIN; CHAIN: A, B, C, D		HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 CAPSID CHAIN:	A, B; ANTIBODY FAB25.3	TOTOMENT, CLEMIN LI, IN, L, IM,		HLA-A 0201; CHAIN: A; BETA-2 MICROGLOBULIN; CHAIN: B;	TAX PEPTIDE; CHAIN: C; T	CHAIN: D. T. CELL. BECEPTOR	BETA; CHAIN: E;	FAB B7-15A2; CHAIN: L, H;		
PDB CHAI STAR END Psi Blast Verify	en de la companya de La companya de la companya de	SEQFOL D score					78.30						295.76		,				
PDB CHAI STAR END Psi Blast D N ID T AA AA AA I		PMF score	1.00	-0.09	66.0	1.00	,		00.1								1.00		
PDB CHAI STAR END Psi Bi	n 1983 Servicios No	Verify score	0.83	0.14	69:0	0.91			0:30								0.48		
PDB CHAI STAR D		Psi Blast	4.5e-40	le-35	1.3e-36	1.5e-37	1.5e-37		1.6e-94		্ব শ্ব ক্ষ		4.8e-64				1.6e-95		
PDB CHAI D N ID N ID		END AA	169	168	169	169	169		249				263				252		
PDB DD 1499s / 12a2u / 2a2u / 1ao7 1 1ao7 1 1ao7 1 1 1aok 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1		STAR T AA	17	56	25	25	25		21				ង				23		
		CHAI N ID	¥		A	Ą	¥.		н				Щ		•		I		
SEQ ID NO: 1758 1758 1758 1759 1759 1759		PDB GI	1qqs	1rbp	2a2u	2a2u	2a2u		lafv				lao7				laqk		
		SEQ NO:	1758	1758	1758	1758	1758		1759				1759				1759	-,	

PDB annotation	PROPENSITY TO CRYSTALLIZE, 3 IMMUNOGLOBULIN	COMPLEX (MHC/VIRAL PEPTIDE/RECEPTOR) HLA A2 HEAVY CHAIN; COMPLEX (MHC/VIRAL PEPTIDE/RECEPTOR)	COMPLEX (MHC/VIRAL PEPTIDE/RECEPTOR) HLA A2 HEAVY CHAIN; COMPLEX (MHC/VIRAL PEPTIDE/RECEPTOR)			CATALYTIC ANTIBODY CATALYTIC ANTIBODY 6D9 CATALYTIC ANTIBODY, ESTER HYDROLYSIS, ESTEROLYTIC, FAB, 2 IMMUNOGLOBULIN		IMMUNOGLOBULIN INTACT IMMUNOGLOBULIN V REGION C
Coumpound		HLA-A 0201; CHAIN: A; BETA-2 MICROGLOBULIN; CHAIN: B; TAX PEPTIDE; CHAIN: C; T CELL RECEPTOR ALPHA; CHAIN: D; T CELL RECEPTOR BETA; CHAIN: B;	HLA-A 0201; CHAIN: A; BETA-2 MICROGLOBULIN; CHAIN: B; TAX PEPTIDE; CHAIN: C; T CELL RECEPTOR ALPHA; CHAIN: D; T CELL RECEPTOR BETA; CHAIN: E;	IMMUNOGLOBULIN 3D6 FAB	IMMUNOGLOBULIN FAB FRAGMENT OF HUMANIZED ANTIBODY 4D5, VERSION 4 1FVD 3	IMMUNOGLOBULIN 6D9; CHAIN: L, H;	COMPLEX (ANTIBODY/BINDING PROTEIN) IGGI FAB FRAGMENT COMPLEXED WITH PROTEIN G (DOMAIN III) IIGC 5 PROTEIN G, STREPTOCOCCUS IIGC 15	IGG2A INTACT ANTIBODY - MAB231; CHAIN: A, B, C, D
SEQFOL D score			386.70					
PMF score		1.00		1.00	1.00	00.1	1.00	66.0
Verify score		0.74		0.30	0.41	0.47	0.21	0.42
Psi Blast		1.2e-98	1.2e-98	9.6e-94	6.4e-96	4.8e-95	1.6e-95	8e-99
END AA		263	263	252	252	252	252	263
STAR T AA		22	22	21	21	21	22	21
CHAI N ID		m	បា	H	B	Н	H	В
PDB ID		15d2	1bd2	1dfb	1fvd	lhyx	ligc	ligt
SEQ ID NO:		1759	1759	1759	1759	1759	1759	1759

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PDB annotation	REGION, IMMUNOGLOBULIN	IMMUNOGLOBULIN, IMMUNOGLOBULIN,	COMPLEX (IMMUNOGLOBULIN/PEPTIDE) IMMUNOGLOBULIN, IGGI; FAB FRAGMENT, CROSSFEACTIVITY,	HIVI PROTEASE, ENZYME 2 INHIBITION, COMPLEX (IMMUNOGLOBULIN/PEPTIDE)	BLOOD COAGULATION, SERINE	PROTEASE, COMPLEX, CO-FACTOR, 2 RECEPTOR ENZYME, INHIBITOR,	GLA, EGF, 3 COMPLEX (SERINE PROTEASE/COFACTOR/LIGAND)	DI ANT DOOTEIN TWO	HOMOLOGOUS HEVEIN-LIKE DOMAINS	SUGAR BINDING PROTEIN UDA;	LECTIN, HEVEIN DOMAIN, UDA, SUPERANTIGEN	SUGAR BINDING PROTEIN UDA;	LECTIN, HEVEIN DOMAIN, UDA,	SOFEWANTIOEN, SACCHANDE BINDING	SIGNALLING PROTEIN BINDING PROTEIN, CYTOKINE, SIGNALLING	PROTEIN	SIGNALLING PROTEIN BINDING PROTEIN, CYTOKINE, SIGNALLING	PROTEIN	BLOOD COAGULATION INHIBITOR
Coumpound		NIG9 (IGGI=LAMBDA=); CHAIN: L, H;	MONOCLONAL ANTIBODY F11.2.32; CHAIN: L, H, M, N; HIV-1 PROTEASE PEPTIDE; CHAIN: P, Q;		BLOOD COAGULATION	SOLUBLE TISSUE FACTOR;	CHAIN: T, U; D-PHE-PHE-ARG- CHLOROMETHYLKETONE OPER CARY, WITH CHAIN; C.	AGGI ITTIMIN ISOI FOTTINI VI:	CHAIN: A	AGGLUTININ ISOLECTIN	VI/AGGLUTININ ISOLECTIN V; CHAIN: A;	AGGLUTIMIN ISOLECTIN	I/AGGLUTININ ISOLECTIN V/	, T. T.	TUMOR NECROSIS FACTOR RECEPTOR; CHAIN: A, B;		TUMOR NECROSIS FACTOR RECEPTOR; CHAIN: A, B;		FLAVORIDIN; IFVL 4 CHAIN:
SEQFOL D score					50.68						,				62.34				
PMF score		1.00	1.00					100		-0.12		0.00					0.36		0.04
Verify score		0.35	0.39	·				0.40		90.0		-0.20					-0.34		-0.37
Psi Blast		1.6e-93	3.2e-93		6e-10			1.1e-07		3e-08		60-99			3e-12		3e-12	,	1.2e-12
END AA		249	251		195			88		88		88			192		203		101
STAR T AA		21	22		29			12	!	12		12			37		57	;	15
CHAI N ID		Н	т Н	•	1			A	<u></u>	¥		¥		-	∢		⋖		
PDB ID		lngp	2hrp		Idan			lehd		leis		len2			lext		lext	:	IM IM
SEQ NO:		1759	1759		1762			1762		1762		1762			1762		1762	0,00	70/1

Day Comment	L D D dilliotation	GP IIB/IIIA ANTAGONIST 1FVL 9	GLYCOPROTEIN GLYCOPROTEIN	GLYCOPROTEIN GLYCOPROTEIN	SIGNALLING PROTEIN TYPE I RECEPTOR, STNFR1; 1NCF 8	BINDING PROTEIN, CYTOKINE INCF 19	SIGNALLING PROTEIN TYPE I	RECEPTOR, STNFRI; INCF 8 BINDING PROTEIN, CYTOKINE	IIVCE IS	COMPLEX (BLOOD COAGULATION/INHIBITOR)	CHRISTIMAS FACTOR; COMPLEX,	INHIBITOR, HEMOPHILIA/EGF,	BLOOD COAGULATION, 2 PLASMA,	SERINE PROTEASE, CALCIUM-	BINDING, HYDROLASE, 3	GLYCOPROTEIN	SERINE PROTEASE INHIBITOR	FACTOR XA INHIBITOR;	ANTISTASIN, CRYSTAL	STRUCTURE, FACTOR XA	INHIBITOR, 2 SERINE PROTEASE	INHIBITOR, THROMBOSIS	SEKINE FROIEASE INFIBITOR	FACTOR AN INTIBILION;	ANTISTASIN, CRYSTAL	SIRUCIONE, FACION AN	NUMBITOR, 2 SERVINE PROTECTION TO PROTECTION THE PROTECTION THE PROTECTION TO PROTECTI	SERVING PROTEST SET THIRD TOP	SEKING PROTECTION OF THE PROTECTION	ANTISTASIN, CRYSTAL
5	Country	NULL IFVL 5	LAMININ; CHAIN: NULL;	LAMININ; CHAIN: NULL;	TUMOR NECROSIS FACTOR RECEPTOR; INCF 4 CHAIN: A,	B; 1NCF 5	TUMOR NECROSIS FACTOR	RECEPTOR; INCF 4 CHAIN: A, B; INCF 5		FACTOR IXA; CHAIN: C, L.; D- PHE-PRO-ARG; CHAIN: I;				****			ANTISTASIN; CHAIN: NULL;					ANTERIOTA CIDI. CHIA INI. NETI 1	ANTISTASIN; CHAIN: NOLL;			•		ANERIOTA CITA DE LA DE LA DELLA DE LA DELLA DE LA DELLA DELL	ANTISTASIN; CHAIN: NOLL;	
TOBO BOT	D score			66.44			55.28		, ,	57.36												26.03	65.63							
20,400	score		-0.12		0.23												0.15									1-5		5 5	71.7	
X7	score		0.17		-0.24												0.05											71.0	-0.1 4	
Dei Diest	E SI DIMST		4.5e-19	1.3e-20	7.5e-09		7.5e-11		,	36-14							3e-17					1 50 10	1.35-10					30.10	07-10	
CIN'S	AA		184	203	140		681		,	9/1							121					161	- - -					161	<u> </u>	
C. Y. L. S	TAA		15	48	11		55			4							61			-		22	<u> </u>					0,5	9	
17100	NED				¥		Ą		T ,	<u> </u>											_									
qua	B		150	1klo	Incf	·	lncf	·	,	χď.							1skz					16/2	1					1 chr	7	
Cab	S E S		1762	1762	1762		1762			707.							1762				-	1763	70					17.63	70.	

PDB annotation	STRUCTURE, FACTOR XA INHBITOR, 2 SERINE PROTEASE INHIBITOR, THROMBOSIS	SERINE PROTEASE INHIBITOR FACTOR XA INHIBITOR; ANTISTASIN, CRYSTAL STRUCTURE, FACTOR XA INHIBITOR, 2 SERINE PROTEASE INHIBITOR, THROMBOSIS		TREFOIL FAMILY OF PEPTIDES PSP REPEAT, GROWTH FACTOR, SIGNAL			SIGNAL TRANSDUCTION PROTEIN	ENDOCYTOSIS/EXOCYTOSIS SYNAPTOTAGMIN, C2-DOMAIN, EXOCYTOSIS, NEUROTRANSMITTER 2 RELEASE, ENDOCYTOSIS/EXOCYTOSIS	ENDOCYTOSIS/EXOCYTOSIS SYNAPTOTAGMIN, C2-DOMAIN, EXOCYTOSIS, NEUROTRANSMITTER 2 RELEASE,
Coumpound		ANTISTASIN; CHAIN: NULL;	MEMBRANE PROTEIN VITELLINE MEMBRANE OUTER LAYER PROTEIN I IVMO 3	PORCINE PANCREATIC SPASMOLYTIC POLYPEPTIDE; CHAIN: A, B;	LECTIN (AGGLUTININ) WHEAT GERM AGGLUTININ (ISOLECTIN 2) 9WGA 3	LECTIN (AGGLUTININ) WHEAT GERM AGGLUTININ (ISOLECTIN 2) 9WGA 3	BETA-SPECTRIN; 1BTN 4 CHAIN: NULL: 1BTN 5	SYNAPTOTAGMIN I, CHAIN: A,	SYNAPTOTAGMIN I; CHAIN: A;
SEQFOL D score	-	·		61.72		97.20	:		1 24 2 42 2 72 2 73 2 74 2 74 2 74 2 74 2 74 2 74 2 74 2 74
PMF score		80:0-	-0.15		0.13		0.70	0.24	0.01
Verify score		0.13	0.36		0.12		-0.02	0.52	0.04
Psi Blast		4.5e-17	9e-33	0.0014	1.5e-18	6e-29	0.003	0.0043	1.2e-11
END		204	190	191	133	191	234	347	349
STAR T AA		86	35	8	13	32	200	245	245
CHAI N ID			Ą	Ą	ď	¥		∢	V
PDB ID		1skz	Ivmo	2psp	9wga	Эмда	19tn	lbyn	1byn
SEQ NO:		1762	1762	1762	1762	1762	1768	1768	1768

PDB annotation	ENDOCYTOSIS/EXOCYTOSIS	ENDOCYTOSIS/EXOCYTOSIS BETA SANDWICH, CALCIUM ION, C2 DOMAIN	SIGNALING PROTEIN DAPP1, PHISH, BAM32; PLECKSTRIN, 3-PHOSPHOINOSITIDES, INOSITOL TETRAKISPHOSPHATE 2 SIGNAL TRANSDUCTION PROTEIN,	SIGNALING PROTEIN DAPPI, PHISH, BAM32; PLECKSTRIN, 3-PHOSPHOINOSITIDES, INOSITOI.	TETRAKISPHOSPHATE 2 SIGNAL TRANSDUCTION PROTEIN, ADAPTOR PROTEIN	SIGNALING PROTEIN NF1-333;	NEUROFIBROMAN, 1 TFE 1 NEUROFIBROMATOSIS, NF1, RAS,	GAP, 2 SIGNAL TRANSDUCTION, CANCER, GROWTH REGULATION.	GTP 3 HYDROL YSIS, PATIENT MUTATION, ARGININE FINGER	SIGNALING PROTEIN NF1-333;	NEUROFIBROMIN, 1 PFE 1 NEUROFIBROMATOSIS, NF1, RAS, GAP, 2 SIGNAL, PRANSOUCTION.	CANCER, GROWTH REGULATION,	GIF 3 HIDROLISIS, FAILENI MUTATION, ARGININE FINGER		
Coumpound	TO THE WATER TO THOUGHT TON	SYNAPIOIAGMIN III; CHAIN: A;	DUAL ADAPTOR OF PHOSPHOTYROSINE AND 3- CHAIN: A;	DUAL ADAPTOR OF PHOSPHOTYROSINE AND 3- CHAIN: A:		NEUROFIBROMIN; CHAIN: A;	-			NEUROFIBROMIN; CHAIN: A;				PHOSPHORYLATION PLECKSTRIN (N-TERMINAL	PLECKSTRIN HOMOLOGY DOMAIN) MUTANT 1PLS 3
SEQFOL D score						108.36	,								
PMF	730	0.54	0.36	0.70						66.0				2E '0	
Verify	i,	0.47	0.07	-0.29	:					0.21				0.33	
Psi Blast	1 5.05	4.56-05	6e-05	9e-06		7.5e-68				7.5e-68				4.5e-05	
END AA	676	302	235	239		289				- 289				239	
STAR T AA	242	747	173	173		400				416				173	
CHAI N ID	\ 	€	∀	Ą		∢.				A		•			
PDB ID	17	, do	Ifao	1fb8		- Gul				1nfi				Ipls	
SEQ ID NO:	1750	1,08	1768	1768	34.	1768				1768				1768	

PDB annotation		SIGNAL TRANSDUCTION SON OF SEVENLESS, PLECKSTRIN, SON OF SEVENLESS, SIGNAL TRANSDUCTION	SIGNAL TRANSDUCTION IRS-1; BETA-SANDWHICH, SIGNAL TRANSDUCTION	HYDROLASE CALB DOMAIN; HYDROLASE, C2 DOMAIN, CALB DOMAIN			GTPASE ACTIVATION GAP-334, GAPETTE; GTPASE ACTIVATION, RAS, GAP, SIGNAL TRANSDUCTION, GROWTH 2 REGIL! A TION CANCER	GTPASE ACTIVATION GAP-334, GAPETTE; GTPASE ACTIVATION, RAS, GAP, SIGNAL TRANSDUCTION, GROWTH 2 REGULATION, CANCER	RNA-BINDING PROTEIN/RNA TRA PRE-MRNA; SPLICING REGULATION, RNP DOMAIN, RNA
Coumpound	WITH LEU GLU (HIS)6 ADDED TO THE C TERMINUS 1PLS 4 (INS(G105-LEHHHHHHH)) (NMR, 25 STRUCTURES) 1PLS 5	SOS 1; CHAIN: NULL;	INSULIN RECEPTOR SUBSTRATE 1; CHAIN: A, B;	PHOSPHOLIPASE A2; CHAIN: NULL;	CALCIUM/PHOSPHOLIPID BINDING PROTEIN SYNAPTOTAGMIN I (FIRST C2 DOMAIN) (CALB) 1RSY 3	CALCIUM/PHOSPHOLIPID BINDING PROTEIN SYNAPTOTAGMIN I (FIRST C2 DOMAIN) (CALB) IRSY 3	P120GAP; CHAIN: NULL;	P120GAP; CHAIN: NULE;	SXL-LETHAL PROTEIN; CHAIN: A, B; RNA (5'- R(P*GP*UP*UP*GP*UP*UP*
SEQFOL D score						-	774	183.05	
PMF score		0.39	0.16	0.22	0.05	0.49	1.00		-0.19
Verify score		-0.48	0.17	0.22	-0.14	0.13	0.62		0.05
Psi Blast		0.00015	3e-05	90- 9 9	0.0043	1.5e-09	1.5e-91	1.5e-91	3.2e-14
END AA		235	245	349	347	349	712	718	205
STAR T AA		162	184	247	245	246	397	397	126
CHAI N ID			Ą		•				A
PDB ED		lpms	1998	ırlw	Irsy	lrsy	l wer	l wer	1b7f
SEQ No:		1768	1768	1768	1768	1768	1768	1768	1770

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PDB annotation C; COMPLEX IN: RNA-BINDING PROTEIN/RNA TRA PRE-MRNA; SPLICING GENE REGULATION/RNA POLY(A) BINDING PROTEIN 1, PABP 1; RRM, PROTEIN-RNA COMPLEX, GENE REGULATION/RNA POLY(A) BINDING PROTEIN 1, PABP 1; RRM, PROTEIN-RNA COMPLEX, GENE REGULATION/RNA N, PROTEIN-RNA COMPLEX, GENE REGULATION/RNA PROTEIN-RNA COMPLEX, GENE PROTEIN-RNA COMPLEX, GENE	
	AP*
Coumpound UP*UP*UP*UP*UP*UP-CHAIN: P. Q; SXL-LETHAL PROTEIN; CHAIN: A, B; RNA (5'- R(P*GP*UP*UP*UP*UP*UP*UP*UP*UP*UP*UP*UP*UP*UP	E, 1, 2, 11, 13, 13, 14, 18, 18, 18, 18, 18, 18, 18, 18, 18, 18
SEQFOL D score	
9.002 -0.02 -0.01 -0.01 -0.11	0.89
Verify score 0.24 0.63 0.63 0.09 0.40 0.07	0.45
Psi Blast 1.6e-37 4.8e-14 4.8e-14 6.4e-34 1.6e-32	6.4e-28
AA 314 431 431 431 431	409
STAR T AA 132 236 236 136 136	238
CHAI N ID A A A A A A A A A A A A A A A A A A	В
PDB 1D7f 1b7f 1b7f 1cvj 1cvj 1cvj	lcvj
SEQ ID NO: 1770 1770 1770 1770 1770 1770 1770 177	1770

PDB CHAI STAR	_	ı	END	Psi Blast	Verify	PMF	SEQFOL Decera	Coumpound	PDB annotation
					31035	31036	arone A		
								R(*AP*AP*AP*AP*AP*AP*AP* AP*AP*AP*AP;3); CHAIN: M, N, O, P, Q, R, S, T;	REGULATION/RNA
Icvj B 352 435		435	ļ	1.6e-12	0.33	0.76		POLYDENYLATE BINDING PROTEIN 1; CHAIN: A, B, C, D,	GENE REGULATION/RNA POLY(A) BINDING PROTEIN 1, PABP 1; RRM,
								E, F, G, H; RNA (5'-	PROTEIN-RNA COMPLEX, GENE
								AP*AP*A)-3); CHAIN: M, N,	KEGOLATION/KINA
10vi E 239 403 6	702	┪	٧	7 7 71	0.13	270		O. P. O. R. S. T.	VAN TOO MANUAL TOOLS THE
204	700			12-21	Š	6.6		PROTEIN 1: CHAIN: A R C D	RINDING PROTFIN 1 PARP 1: RRM
								E, F, G, H; RNA (5'-	PROTEIN-RNA COMPLEX, GENE
								R(*AP*AP*AP*AP*AP*AP*	REGULATION/RNA
								AP*AP*AP*A)-3'); CHAIN: M, N,	
		7	_]					O, P, Q, R, S, T;	
lcvj H 238 405 1.6	405		1.6	1.6e-2i	0.03	0.25		POLYDENYLATE BINDING	GENE REGULATION/RNA POLY(A)
California								PROTEIN 1; CHAIN: A, B, C, D,	BINDING PROTEIN 1, PABP 1; RRM,
								E, F, G, H; RNA (5'-	PROTEIN-RNA COMPLEX, GENE
								R(*AP*AP*AP*AP*AP*AP*	REGULATION/RNA
								AP*AP*AP*A)-3'); CHAIN: M, N,	
11 250 425	307	1	-	5	0.70	0,70		0, F, Q, K, S, I;	Charles and a straightful management
326	45		<u>-</u>	71-20-1	0	0.00		PROTEIN 1. CHAIN: A B C D	GENE KEGULATION/KNA FOLY(A)
								E, F, G, H; RNA (5'-	PROTEIN-RNA COMPLEX, GENE
				7				R(*AP*AP*AP*AP*AP*AP*	REGULATION/RNA
					•			AP*AP*AP*A)-3'); CHAIN: M, N,	
		1						O, P, Q, R, S, T;	
A 233 322	322		3.	3.2e-21	0.04	0.19		HU ANTIGEN C; CHAIN: A;	RNA BINDING PROTEIN RNA- BINDING DOMAIN
1d8z A 346 431 4	431		4	4.8e-13	0.52	0.27		HU ANTIGEN C; CHAIN: A;	RNA BINDING PROTEIN RNA- RINDING DOMAIN
1d9a A 136 218 8	218		-	8e-14	0.03	-0.19		HU ANTIGEN C; CHAIN: A;	RNA BINDING PROTEIN RNA-
				,	,				BINDING DOMAIN
1d9a A 237 319	319	\neg		3.2e-18	0.48	-0.03		HU ANTIGEN C; CHAIN: A;	RNA BINDING PROTEIN RNA-

_	,					 -																		-					, <u>-</u>	
PDB annotation	BINDING DOMAIN	RIBONUCLEOPROTEIN UIA117; RIBONUCLEOPROTEIN, RNP	DOMAIN, SPLICEOSOME	STRUCTURAL PROTEIN PROTEIN	C23; RNP, RBD, RRM, RNA BINDING DOMAIN, NIICLEOLIIS	NUCLEAR PROTEIN	HETEROGENEOUS NUCLEAR	RIBONUCLEOPROTEIN A1,	NUCLEAR PROTEIN, HNRNP, RBD,	RRM, RNP, RNA BINDING, 2	NEIGH EAR PROTEIN	NUCLEAR FROIDING	HETEROGENEOUS NUCLEAR	KIBONUCLEOPROTEIN A1,	NUCLEAR PROTEIN, HNRNP, RBD,	RRM, RNP, RNA BINDING, 2	RIBONUCLEOPROTEIN	NUCLEAR PROTEIN HETEBOGENEOUS NUCLEAR	DIBONITOI EORDONIN A 1	KIBUNUCLEUFKU EIN A1,	NUCLEAR PROTEIN, HNRNP, RBD,	RKM, KNP, KNA BINDING, Z RIBONI ICI EOPROTHIN	RNA BINDING PROTEIN RNA-	BINDING DOMAIN		RNA BINDING PROTEIN RNA-	BINDING DOMAIN		RNA BINDING PROTEIN RNA-	BINDING DOMAIN
Coumpound		UI SMALL NUCLEAR RIBONUCLEOPROTEIN A:	CHAIN: NULL;	NUCLEOLIN RBD2; CHAIN: A;		HNRNP A1; CHAIN: NULL:					Think to city but it	MINNAY AI; CHAIN: NOLL;		•				HNRNP A1; CHAIN: NULL;		-	٠.		HETEROGENEOUS NUCLEAR	RIBONUCLEOPROTEIN D0:	CHAIN: A;	HETEROGENEOUS NUCLEAR	RIBONUCLEOPROTEIN DO;	CHAIN: A;	HETEROGENEOUS NUCLEAR	KIBONUCLEOPROTEIN DO; CHAIN: A:
SEQFOL D score					-					-															:		-			
PMF		0.12		0.07		-0.09					200	0.73						0.94					-0.19			0.16		-	0.68	
Verify score		0.57		0:30		0.17					100	17.0						0.83					0.03			0.78			0.91	
Psi Blast		1.5e-11		3.2e-12		4.8e-45					1 62 40	1.05-40						1.3e-16					6.4e-20			4.8e-22			9.6e-15	•
END AA		315		313		314					307	3						431					213			314			425	
STAR T AA		230		222		129					33.1	<u>.</u>			-			350					136			237			351	
CHAI N ID				¥												•					***	,	A			Ą			∢	
PDB ID		1fbt		1fjc		lhal				·-···	140.1	11101						lhal					1hd1			1hd1			lhd1	
SEQ NO:		0221		1770		1770				- N - 1 - 1	1770	2						1770					1770			1770			1770	

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PDB annotation	RIBONUCLEOPROTEIN PTB, PTB- C198, HETEROGENEOUS NUCLEAR POLYPYRIMIDINE TRACT BINDING PROTEIN, RNP, RNA, SPICING, 2 TRANSLATION			RNA BINDING PROTEIN RNA- BINDING DOMAIN	RNA BINDING PROTEIN RNA- BINDING DOMAIN	RNA BINDING PROTEIN RNA-BINDING DOMAIN	RNA-BINDING DOMAIN RNA- BINDING DOMAIN, ALTERNATIVE SPLICING	RNA-BINDING DOMAIN RNA- BINDING DOMAIN, ALTERNATIVE SPLICING	RNA-BINDING PROTEIN SPLICING,
Coumpound	POL YP YRIMIDINE TRACT- BINDING PROTEIN; CHAIN: A;	RNA-BINDING PROTEIN SEX- LETHAL PROTEIN (C- TERMINUS, OR SECOND RNA- BINDING DOMAIN 1SXL 3 (RBD-2), RESIDUES 199 - 294 PLUS N-TERMINAL MET) 1SXL 4 (NMR, 17 STRUCTURES) 1SXL 5	RNA-BINDING PROTEIN SEX- LETHAL PROTEIN (C- TERMINUS, OR SECOND RNA- BINDING DOMAIN 15XL 3 (RBD-2), RESIDUES 199 - 294 PLUS N-TERMINAL MET) 15XL 4 (NMR, 17 STRUCTURES) 15XL 5	MUSASHII; CHAIN: A;	MUSASHII; CHAIN: A;	MUSASHII; CHAIN: A;	SEX-LETHAL PROTEIN; CHAIN: NULL;	SEX-LETHAL PROTEIN; CHAIN: NULL;	SPLICING FACTOR U2AF 65 KD
SEQFOL D score									
PMF score	0.15	-0.15	0.13	-0.18	0.17	66.0	0.25	0.70	0.88
Verify score	0.06	0.21	0.51	0.11	0.74	0.91	0.36	0.42	0.75
Psi Blast	4.8e-19	1.6e-18	3.2e-13	1.3e-14	6.4e-19	4.8e-14	1.1e-19	4.8e-14	6.4e-18
END AA	427	319	429	213	314	425	322	431	314
STAR T AA	238	223	341	136	237	351	236	348	236
CHAI N ID	₹			A	4	A	•		Ą
PDB ID	1 1 1 1 1 1 1 1 1	lsxl	1sxl	2mss	2mss	2mss	2sxl	2sxl	2u2f
SEQ ID NO:	1770	1770	1770	1770	1770	1770	1770	1770	1770

PDB annotation	U2 SNRNP, RBD, RNA-BINDING PROTEIN	COMPLEX	(KIBON UCLEOPKO I ELIVIDNA) HNRNP A1, UPI; COMPLEX	(RIBONUCLEOPROTEIN/DNA),	HEIEROGENEOUS NUCLEAR 2 RIBONUCLEOPROTEIN A1	COMPLEX	(KIBONOCLEOFKOIEIN/DINA)	(RIBONUCLEOPROTEIN/DNA),	HETEROGENEOUS NUCLEAR 2	RIBONUCLEOPROGREDIA	RNA BINDING DOMAIN RNA	BINDING DOMAIN, RBD, RNA	RECOGNITION MOTIF, RRM, 2	SPLICING INHIBITOR,	TRANSLATIONAL INHIBITOR, SEX 3	DETERMINATION, X CHROMOSOME	DOSAGE COMPENSATION	RNA BINDING DOMAIN RNA	BINDING DOMAIN, RBD, RNA	RECOGNITION MOTIF, RRM, 2	SPLICING INHIBITOR,	TRANSLATIONAL INHIBITOR, SEX 3	DETERMINAȚION, X CHROMOSOME	DOSAGE COMPENSATION		COMPLEX (ZINC FINGER/DNA)	COMPLEX (ZINC FINGER/DNA),	PROTEIN	COMPLEX (ZINC FINGER/DNA) ZINC
Coumpound	SUBUNIT; CHAIN: A;	HETEROGENEOUS NUCLEAR	CHAIN: A; 12-NUCLEOTIDE	SINGLE-STRANDED	IELUMEIKIC DINA; CHAIN; B;	HETEROGENEOUS NUCLEAR	CHAIN: A: 12-NIICI EOTIDE	SINGLE-STRANDED	TELOMETRIC DNA; CHAIN: B;		SEX-LETHAL; CHAIN: A, B, C;							SEX-LETHAL; CHAIN: A, B, C;								OGSR ZINC FINGER PEPTIDE;	CHAIN: A; DUPLEX Of IGONITICE FORTING	SITE; CHAIN: B, C;	DNA; CHAIN: A, B, D, E;
SEQFOL D score		-																								74.27			
PMF		0.09				0.52		• •			0.02							96.0											0.04
Verify		0.00			·	09:0	,	-			0.22							0.32											-0.22
Psi Blast		4.8e-47				1.6e-43					3.2e-36							1.4e-32								3.2e-31			9.6e-44
END		319				433					307				-	-		425					•			2			219
STAR T AA		128				ឌ					133							236							3,5	303			138
CEAI N ID		¥				4					٧,	•						₩.								∢			S
PDB ID		2up]				2up1					383			,			,	3sxl								Iain			Imey
SEQ ID NO:		1770				1770					0241							1770							. 4.40	7//1			1772

PDB annotation	FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUETORE, COMPLEX (ZINC FINGER/DNA)	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
Coumpound	CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;
SEQFOL D score						1 - 11 1 - 2 - 2 - 2	
PMF		96.0	00'1	1.00	1.00	1.00	1.00
Verify score		0.35	0.14	0.54	0.24	0.71	0.74
Psi Blast		4.8e-46	4.8e-47	1.3e-47	3.2e-48	1,1e-49	3.2e-50
END		247	275	303	331	359	387
STAR T AA		166	194	222	250	278	306
CHA! N ID		ပ	ပ	O	Ų	ن د	ن
PDB ID		Imey	Imey	Ітеу	Imey	Imey	1mey
SEQ ID NO:		1772	1772	27.21	1772	1772	1772

	NA) ZINC ESIGN, 2 MPLEX	NA) ZINC ESIGN, 2 MPLEX	NA) ZINC ESIGN, 2 MPLEX	NA) ZINC ESIGN, 2 MPLEX	NA) ZINC BSIGN, 2 MPLEX	NA) ZINC ESIGN, 2 MPLEX	NA) ZINC
PDB annotation	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX CONF FINGEP, DNA A	CONTRACTOR OF THE COMPLEX COMP	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2
	OEADS	OEAUS	SEADE	SE Z D D	SEZE	SEAGE	SER
Coumpound	DNA; CHAIN; A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN: CHAIN: C, F, G:
SEQFOL D score						102.60	
PMF	00:	1.00	1.00	1.00	1.00		1.00
Verify score	69.0	-0.02	0.37	0.52	0.31		60.0
Psi Blast	1.6e-51	4.8e-51	9.6e-51	1.6e-50	1.6e-50	1.6e-50	6.4e-34
END	415	443	471	499	527	528	531
STAR T AA	334	362	390	418	446	446	474
CHAI N ID	ပ	v	O	ပ	၁	υ .	ပ
FDB CI	lmey	Imey	Imey	Imey	Ітеу	1mey	Imey
SEQ NO.	1772	1772	1772	1772	1772	1772	1772

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PDB annotation	(ZINC FINGER/DNA)	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA	INTERACTION, PROTEIN DESIGN, 2	CRYSTAL STRUCTURE, COMPLEX	COMPLEX (ZINC FINGER/DNA) ZINC	FINGER, PROTEIN-DNA	INTERACTION, PROTEIN DESIGN, 2	CRYSTAL STRUCTURE, COMPLEX	(ZINC FINGER/DINA)	COMPLEX (TRANSCRIPTION PEGIT ATTOMONA) COMPLEY	(TRANSCRIPTION	REGULATION/DNA), RNA	POLYMERASE III, 2	TRANSCRIPTION INITIATION, ZINC	FUNCENT NOTESIN	COMPLEX (TRANSCRIPTION	REGULATION/DNA) COMPLEX	REGIT ATTON/ONA) RNA	POI VMERASE III 2	TE ANSCRIPTION INITIATION ZINC	FINGER PROTEIN	COMPLEX (TRANSCRIPTION	REGULATION/DNA) COMPLEX	(TRANSCRIPTION)	REGULATION/DNA), RNA	POLYMERASE III, 2	TRANSCRIPTION INITIATION, ZINC	FINGER PROTEIN	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX
Coumpound		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER	PROTEIN; CHAIN: C, F, G;		DNA: CHAIN: A. B. D. E.	CONSENSUS ZINC FINGER	PROTEIN; CHAIN: C, F, G;			TFIIIA; CHAIN: A, D; 5S RIBOSOMAI RNA GENE:	CHAIN: B. C. E. F.		,			TFIIIA; CHAIN: A, D; 58	KIBOSOMAL RNA GENE;	CHAIN: D, C, L, 1,	-			TFIIIA; CHAIN: A, D; 5S	RIBOSOMAL RNA GENE;	CHAIN: B, C, E, F;					TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE;
SEQFOL D score											-												,				V. 1. 4.		100.49
PMF score		0.05		,	0.29					0.54					,	8						0.99	:				, .		
Verify score		0.55			-0.73					0.24			_		000	0.28						0.07	-	. :		, ;			
Psi Blast		9.6e-11			1.6e-09					1.3e-35		,	-		20.	4.8e-37			_			3.2e-38							3.2e-38
END		161	-		71					312					9	368						452							497
STAR T AA		164			4					167					222	577						307							334
CHAI N ID		Ð			U	·				∢						<						Ą				•			٧
PDB ID		1mey			Imev	•				1476					191	o <u>n</u>						1116	:						1 4f 6
SEQ ID NO:		1772			1772					1772					1777	11.12						1772	٠,						1772

PDB annotation	(TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INTIATION, ZINC FINGER PROTEIN	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION
Coumpound	CHAIN: B, C, E, F;	TFIIIA; CHAIN: A, D; 58 RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	TFIIIA; CHAIN: A, D; SS RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	YYI; CHAIN: C; ADENO- ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	YYI; CHAIN: C; ADENO- ASSOCIATED VIRUS PS INITIATOR ELEMENT DNA; CHAIN: A, B;
SEQFOL D score					
PMF		0.95	0.94	0.11	0.72
Verify score		-0.06	0.01	0.07	-0.21
Psi Blast		1.6e-37	1.4e-36	4.8e-32	1.5e-23
END		509	529	247	275
STAR T AA		363	391	143	169
CHAI N ID		A	∢	ن ن	O
PDB ID		11g	1466	lubd	lubd
SEQ ID NO:	4444	1772	1772	1772	1772

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PDB annotation	(REGULATION/DNA)	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG I, TRANSCRIPTION INITIATION.	INITIATOR ELEMENT TT1, ZINC2	FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX	(TRANSCRIPTION REGULATION/DNA)	COMPLEX (TRANSCRIPTION	REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION,	INITIATOR ELEMENT, YY1, ZINC 2	FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX	(TRANSCRIPTION PEGIT ATTOMONA)	COMPLEX (TRANSCRIPTION	REGULATION/DNA) YING-YANG 1;	TRANSCRIPTION INITIATION,	INITIALOR ELEMBNI, YYI, ZINCZ	PECOGNITION 2 COMPLEX	(TRANSCRIPTION	REGULATION/DNA)	COMPLEX (TRANSCRIPTION	REGULATION/DNA) YING-YANG 1;	TRANSCRIPTION INITIATION,	INITIATOR ELEMENT, YY1, ZINC 2	FINGER PROTEIN, DNA-PROTEIN	RECOGNITION, 3 COMPLEX	(TRANSCRIPTION	COMPLEX (TRANSCRIPTION
Coumpound		YYI; CHAIN: C; ADENO- ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA;	CHAIN: A, B;			YY1; CHAIN: C; ADENO-	ASSOCIATED VIRUS PS INITIATOR ELEMENT DNA;	CHAIN: A, B;			YY1: CHAIN: C: ADENO.	ASSOCIATED VIRUS P5	INITIATOR ELEMENT DNA;	CHAIN: A, B;			,	YYI; CHAIN: C; ADENO-	ASSOCIATED VIRUS P5	INITIATOR ELEMENT DNA;	CHAIN: A, B;				YY1; CHAIN: C; ADENO-
SEQFOL D score			:																		-			-	
PMF score		1.00				1.00					1.00							1.00							1.00
Verify score		0.13			:	0.02			::.:		0.21							0.36							0.03
Psi Blast		4.5e-43			-	1.6e-32					1.5e-46	,						4.8e-34							1.5e-50
END		303				303					359							359							443
STAR T AA		199				202					223							258		-			_		332
CHAI N ID		O		•		U					U	-						ပ ပ							S
PDB CI		1ubd		_		1nbd					lubd							Jubd	****			_			1nbd
SEQ ID NO:		1772				1772					1772							1772	This comment						1772

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REGULATION/DNA) YING-YANG I; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION,
ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	YY I; CHAIN: C; ADENO- ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	YYI; CHAIN: C; ADENO- ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	YYI; CHAIN: C; ADENO- ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA;
				82.44
-	90.1	0.90	00:1	
	0.06	-0.01	0.01	
·	6e-52	96-51	3e-50	9e-51
	472	499	527	528
	360	388	416	420
	၁	ට	O	O
	lubd	Iubd	lubd	Iubd
	1772	1772	1772	1772
	LEMENT DNA;	1ubd C 360 472 6e-52 0.06 1.00 YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 Indianal C; ADENO-ASSOCIATED VIRUS P	1ubd C 360 472 66-52 0.06 1.00 YYI; CHAIN: C; ADENO-ASSOCIATED VRUS P5 NITTATOR ELEMENT DNA; CHAIN: C, ABENO-ASSOCIATED VRUS P5 NITTATOR ELEMENT DNA; CHAIN: C, ADENO-ASSOCIATED VRUS P5 1ubd C 388 499 96-51 -0.01 0.90 YYI; CHAIN: C; ADENO-ASSOCIATED VRUS P5 NITTATOR ELEMENT DNA; CHAIN: A, B; CHAIN: A, B; CHAIN: A, B;	1ubd C 360 472 66-52 0.06 1.00 NY1; CHAIN: C; ADENO-ASSOCIATED VIRUS PS

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PDB annotation	INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATIONDNA)	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INTIATION, INTIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)	TRANSCRIPTION REGULATION TRANSCRIPTION REGULATION, ADRI, ZINC FINGER, NWR	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)	COMPLEX (DNA-BINDING PROTEINDNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA- BINDING PROTEINDNA)	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)	COMPLEX (DNA-BINDING PROTEINIDNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEINIDNA)	COMPLEX (DNA-BRE-FRIG PROTEIN/DNA) FIVE-FINGER GLI;
Coumpound	CHAIN: A, B;	YYI; CHAIN: C; ADENO- ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	ADRI; CHAIN: NULL;	ZINC FINGER PROTEIN GLII; CHAIN: A; DNA; CHAIN: C, D;	ZINC FINGER PROTEIN GLII; CHAIN: A; DNA; CHAIN: C, D;	ZINC FINGER PROTEIN GLII; CHAIN: A; DNA; CHAIN: C, D;	ZINC FINGER PROTEIN GLII; CHAIN: A; DNA; CHAIN: C, D;	ZINC FINGER PROTEIN GLII; CHAIN: A; DNA; CHAIN: C, D;
SEQFOL D score						-		
PMF		1.00	-0.18	0.13	0.95	1.00	0.99	86.0
Verify		0.11	0.11	-0.10	0.26	0.51	0.21	0.31
Psi Blast		8e-35	8e-14	3.2e-29	3e-58	9e-64	1.5e-63	1.5e-67
END AA		527	193	246	389	417	445	501
STAR T AA		426	139	102	197	278	306	362
CHAI N ID		ပ		Ą	¥	¥	Ą	Ą
80g C1		lubd	2adr	2gli	2gli	2gli	2gli	2gli
SEQ No.		1772	1772	1772	1772	1772	1772	1772

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PDB annotation	GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA- BINDING PROTEIN/DNA)	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA- BINDING PROTEIN/DNA)	TRANSCRIPTION REGULATION PROTO-ONCOGENE, NUCLEAR BODIES (PODS), LEUKEMIA, 2 TRANSCRIPTION RECEGNATION			LIGASE CBL, UBCH7, ZAP-70, E2, UBIQUITIN, E3, PHOSPHORYLATION, 2 TYROSINE KINASE, UBIQUITINATION, PROTEIN DEGRADATION,	LIGASE CBL, UBCH7, ZAP-70, E2,
Compound		ZINC FINGER PROTEIN GLII; CHAIN: A; DNA; CHAIN: C, D;	ZINC FINGER PROTEIN GLII; CHAIN: A; DNA; CHAIN: C, D;	ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	TRANSCRIPTION FACTOR PML; CHAIN: NULL;	VIRUS EQUINE HERPES VIRUS- 1 (C3HC4, OR RING DOMAIN) 1CHC 3 (NMR, 1 STRUCTURE) 1CHC 4	VIRUS EQUINE HERPES VIRUS- 1 (C3HC4, OR RING DOMAIN) 1CHC 3 (NMR, 1 STRUCTURE) 1CHC 4	SIGNAL TRANSDUCTION PROTEIN CBL; CHAIN: A; ZAP- 70 PEPTIDE; CHAIN: B; UBIQUITIN-CONJUGATING ENZYME E12-18 KDA UBCH7; CHAIN: C	SIGNAL TRANSDUCTION
SEQFOL D score		88.77					, ·		
PMF score			0.84	00.1	0.07	0.52	0.39	0.41	0.21
Verify score			-0.07	0.24	-0.87	-0.50	-0.28	0.41	-0.34
Psi Blast		1.5e-67	1.5e-49	1.6e-34	4.8e-06	1.3e-11	3.2e-06	1.2e-12	3.2e-06
END		501	524	529	59	59	• •	69	59
STAR T AA		362	390	398	10	11	<u>5</u> I	41	15
CHAI N ID		¥	¥	A		•		∀	A
PDB ID		2gli	2gli	2gli	1bor	1chc	Iche	1fbv	1fbv
SEQ D NO:		1772	1772	1772	1774	1774	1774	1774	1774

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PDB annotation	UBIQUITIN, E3, PHOSPHORYLATION, 2 TYROSINE KINASE, UBIQUITINATION, PROTEIN DEGRADATION,	ZINC-BINDING PROTEIN ZINC- BINDING PROTEIN, XNFZ, BEDX, DEVELOPMENT, 3 MID-BLASTULA- TRANSITION	METAL BINDING PROTEIN RING FINGER PROTEIN MAT1; RING FINGER (C3HC4)	CONTRACTILE PROTEIN TRIPLE- HELIX COILED COIL, CONTRACTILE PROTEIN	DNA-BINDING PROTEIN V(D)J RECOMBINATION ACTIVATING PROTEIN I; RAG1, V(D)J RECOMBINATION, ANTIBODY, MAD, RING FINGER, 2 ZINC BINUCLEAR CLUSTER, ZINC FINGER, DNA-BINDING PROTEIN	DNA-BINDING PROTEIN V(D)J RECOMBINATION ACTIVATING PROTEIN 1; RAG1, V(D)J RECOMBINATION, ANTIBODY, MAD, RING FINGER, 2 ZINC BINUCLEAR CLUSTER, ZINC FINGER, DNA-BINDING PROTEIN	STRUCTURAL PROTEIN TWO REPEATS OF SPECTRIN, ALPHA HELICAL LINKER REGION, 22 TANDEM 3-HELIX COILED-COILS,
Coumpound	PROTEIN CBL; CHAIN: A; ZAP- 70 PEPTIDE; CHAIN: B; UBIQUITIN-CONJUGATING ENZYME E12-18 KDA UBCH7; CHAIN: C;	NUCLEAR FACTOR XNF7; CHAIN: NULL;	CDK-ACTIVATING KINASE ASSEMBLY FACTOR MAT1; CHAIN: A;	HUMAN SKELETAL MUSCLE ALPHA-ACTININ 2; CHAIN: A;	RAGI; CHAIN: NULL;	RAGI; CHAIN: NULL;	ALPHA SPECTRIN; CHAIN: A, B, C;
SEQFOL D score				54.69			·
PMF score		0.36	0.74	: 	0.84	0.01	0.19
Verify score		-0.23	0.21		-0.03	-0.19	-0.07
Psi Blast		1.5e-13	4.5e-14	3e-06	4.5e-20	6.4e-14	4.5e-07
END		128	70	304	100	109	414
STAR T AA		86	=	છ	11	σ _ν	248
CHAI N ID			A	¥			¥
PDB ID		1 fre	1g25	1quu	1rmd	Irmá	lcun
SEQ ID NO:		1774	1774	1774	1774	1774	1775

PDB annotation	STRUCTURAL PROTEIN	STRUCTURAL PROTEIN TWO REPEATS OF SPECTRIN, ALPHA HELICAL LINKER REGION, 2 2 TANDEM 3-HELIX COILED-COILS, STRIIGTHIRAL PROTEIN	ENDOCYTOSIS/EXOCYTOSIS SYNAPTOTAGMIN ASSOCIATED 35 KDA PROTEIN, P35A, THREE HELIX BUNDLE		TRANSCRIPTION HELIX-BUNDLE	TRANSCRIPTION TRANSCRIPTION, RNA POLYMERASE II SUBUNIT, RPB9, ZN RIBBON, 2 HYPERTHERMOPHILIC, EXTREMOPHILE		
Conmpound		ALPHA SPECTRIN; CHAIN: A, B, C;	SYNTAXIN-1A; CHAIN: A, B, C;	VIRUS EQUINE HERPES VIRUS. 1 (C3HC4, OR RING DOMAIN) 1CHC 3 (NMR, 1 STRUCTURE) 1CHC 4	TRANSCRIPTION ELONGATION FACTOR S-II; CHAIN: A;	RNA POLYMERASE II; CHAIN: NULL;	TRANSCRIPTION REGULATION TRANSCRIPTIONAL ELONGATION FACTOR SII (TFIIS, NUCLEIC-ACID 1TFI 3 BINDING DOMAIN) (NMR, 12 STRUCTURES) 1TFI 4	TRANSCRIPTION REGULATION TRANSCRIPTIONAL ELONGATION FACTOR SII
SEQFOL D score								
PMF score		-0.13	-0.12	0.18	0.52	0.51	1.00	0.75
Verify		0.34	0.10	0.21	-0.14	-0.51	0.16	-0.07
Psi Blast		9e-10	4.5e-09	0.0006	4.5e-06	0.00045	1.6e-10	4.5e-11
END		93	124	553	78	343	345	343
STAR T AA		panel .	6	516	-	291	286	287
CHAI N ID		A	Ą		∢			
PDB ID		lcun	lez3	lchc	leoO	lqyp	H	14fi
SEQ ID NO:		1776	1776	1777	1780	1780	1780	1780

CHAI STAR END NID TAA AA	STAR		AA AA	[Psi Blast	Verify	PMF	SEQFOL D score	Coumpound	PDB annotation
									(TFIIS, NUCLEIC-ACID 1TFI 3 BINDING DOMAIN) (NMR, 12 STRUCTURES) 1TFI 4	
			7							
A 458 510 1.5e-14	. 458 510 1.5e-1	510 1.5e-1	1.5e-1	1.5e-14		-0.85	10.0		EPS8; CHAIN: A, B;	SIGNAL TRANSDUCTION SRC HOMOLOGY DOMAIN; SIGNAL TRANSDUCTION, SH3 DOMAIN, EPS8, PROLINE RICH PEPTIDE
436 507 3e-14	507	507		3e-14		0.30	0.82		ITK; CHAIN: NULL;	TRANSFERASE IL-2-INDUCIBLE T- CELL KINASE; TRANSFERASE, REGULATORY INTRAMOLECULAR COMPLEX, KINASE
459 508 1.2e-11	208	208		1.2e-11		-0.29	0.92		ABL TYROSINE KINASE; CHAIN: NULL;	KINASE KINASE, SH3 DOMAIN, TRANSFERASE, PHOSPHOTRANSFERASE, 2 PROTO- ONCOGENE, MULTIPLE DOMAIN,
A 459 508 Ie-il	459 508	508		[6-1]		-0.27	0.84		ABL TYROSINE KINASE; CHAIN: A, C, E, G; PEPTIDE P41; CHAIN: B, D, F, H;	COMPLEX (TRANSFERASE/PEPTIDE) COMPLEX (TRANSFERASE/PEPTIDE), SIGNAL TRANSDUCTION, 2 SH3 DOMAIN
A 459 508 4.5e-12	459 508 4.5e-1	508 4.5e-1	4.5e-1	4.5e-12		-0.27	1.00		HEMOPOIETIC CELL KINASE; CHAIN: A, B, C, D, E, F;	TRANSFERASE TYROSINE-PROTEIN KINASE, TRANSFERASE, SIGNAL TRANSDUCTION, 2 SH3
A 48 148 0.003	48 148	148		0.003		-0.04	0.63		NUMB PROTEIN; CHAIN: A; NUMB ASSOCIATE KINASE; CHAIN: B;	SIGNALING PROTEIN/TRANSFERASE NAK; COMPLEX, SIGNAL TRANSDUCTION, PHOSPHOTYROSINE BINDING 2 DOMAIN (PTB), ASYMMETRIC CELL DIVISION
A 459 507 6e-11	459 507	507		6e-i1	L	-0.15	1.00		FYN TYROSINE KINASE; CHAIN: A, C; HIV-1 NEF	COMPLEX (SH3 DOMAIN/VIRAL ENHANCER) SROME ENCOGY 3

PDB annotation	DOMAIN; COMPLEX (SH3 DOMAINVIRAL ENHANCER), PROTO-ONCOGENE, 2 TRANSFERASE, TYROSINE- PROTEIN KINASE, PHOSPHORYLATION, 3 AIDS, MYRISTYLATION, GTP-BINDING, ATP-BINDING, SH3 DOMAIN, 4 SH2 DOMAIN, PPII HELIX, PXXP MOTTE	TRANSFERASE PROTO-ONCOGENE TYROSINE KINASE; PROTO- ONCOGENE, TRANSFERASE, TYROSINE-PROTEIN KINASE, 2 PHOSPHORYLATION, ATP-BINDING, MYRISTYLATION, SH3 DOMAIN, 3 COMPLEX (PHOSPHOTRANSFERASE/PEPTIDE)	COMPLEX (SIGNAL TRANSDUCTION/PEPTIDE) COMPLEX (SIGNAL TRANSDUCTION/PEPTIDE), SH3 DOMAIN		COMPLEX (KINASE/PEPTIDE)
Coumpound	PROTEIN; CHAIN: B, D;	PHOSPHOTRANSFERASE FYN; CHAIN: A; 3BP-2; CHAIN: B;	GRB2; CHAIN: A; SOS-1; CHAIN: B;	SIGNAL TRANSDUCTION PROTEIN GROWTH FACTOR RECEPTOR-BOUND PROTEIN 2 (GRB2, N-TERMINAL 1GBR 3 SH3 DOMAIN) COMPLEXED WITH SOS-A PEPTIDE 1GBR 4 (NMR, 29 STRUCTURES) 1GBR 5	P56==LCK== TYROSINE KINASE; ILCK 7 CHAIN: A; ILCK 8 TAIL PHOSPHOPEPTIDE TEGQ(PHOSPHO)YQPQPA;
SEQFOL D score		3,1,2			
PMF score		1.00	0.84	0.74	0.01
Verify score		0.07	-0.33	-0.35	-0.41
Psi Blast		16-11	1.46-12	3e-13	4.8e-19
END AA		508	508	510	581
STAR T AA		457	454	446	456
CHAI N ID		A	Ą	4	A
PDB ID		1fyn	1gbq	1gbr	11ck
SEQ ID NO:		1781	1781	1781	1781

SEO	PDB	CHAI	STAR	END	Psi Blast	Verify	PMF	SEQFOL	Coumpound	PDB annotation
ΑÖ	A ———	A	TAA	AA		score	score	D score		
									1LCK 14 CHAIN: B; 1LCK 15	
1781	Inlo	O .	459	507	36-11	0.18	1.00		C-SRC; CHAIN: C; NL1 (MN7- MN2-MN1-PLPPLP); CHAIN: N;	COMPLEX (TRANSFERASE/PEPTIDE) SRC, SH3 DOMAIN, LIGANDS, NON-PEPTIDE ELEMENTS, 2 COMPLEX (TDANSEED & SEMEPTIDE)
1781	1pwt		457	508	3e-10	0.21	1.00		ALPHA SPECTRIN; CHAIN: NULL;	CIRCULAR PERMUTANT PWT; CIRCULAR PERMUTANT, SH3 DOMAIN, CYTOSKELETON
1781	Iqcf	Ą	456	581	3.2e-18	-0.31	0.15		HAEMATOPOETIC CELL KINASE (HCK); CHAIN: A;	TYROSINE KINASPERCENE KINASE-INHIBITOR COMPLEX, DOWN-REGULATED KINASE, 2 ORDERED ACTIVATION LOOP
1781	Iqkw	Ą	457	208	1.5e-10	0.20	1.00		ALPHA II SPECTRIN; CHAIN: A;	CYTOSKELETON CYTOSKELETON, MEMBRANE, SH3 DOMAIN
1781	lq!y	¥	455	508	3 c -12	-0.05	0.81		TYROSINE-PROTEIN KINASE BTK; CHAIN: A;	TYROSINE-PROTEIN KINASE BRUTONS TYROSINE KINASE, B CELL PROGENITOR KINASE, TRANSFERASE, TYROSINE- PROTEIN KINASE, PHOSPHORYLATION, 2 SH3 DOMAIN
1781	1shf	∢	459 ·	508	7.5e-11	-0.64	00'1		PHOSPHOTRANSFERASE FYN PROTO-ONCOGENE TYROSINE KINASE (E.C.2.7.1.112) 1SHF 3 (SH3 DOMAIN) 1SHF 4	
1781	2лтр	4	27	153	3e-12	0.25	0.64		NUMB PROTEIN; CHAIN: A; GPPY PEPTIDE; CHAIN: B;	CELL CYCLE/GENE REGULATION COMPLEX, SIGNAL TRANSDUCTION, PHOSPHOTYROSINE BINDING 2 DOMAIN (PTB), ASYMETR IC CELL DIVISION, CELL CYCLE/GENE 3 REGULATION
1781	4hck		455	508	7,5e-12	0.46	1.00		HEMATOPOIETIC CELL	TRANSFERASE HCK; SH3, PROTEIN

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PDB annotation	TYROSINE KINASE, SIGNAL TRANSDITCTION 2 TRANSFERASE		COMPLEX (TRANSCRIPTION FACTOR/DNA) TRANSCRIPTION	FACTOR, PROTEIN-DNA COMPLEX,	COMPLEX (TRANSCRIPTION FACTOR/DNA)	LIPID BINDING PROTEIN APO-E3;	LIPID TRANSPORT, LIPID	TRANSPORT, HEPARIN-BINDING, PLASMA 2 PROTEIN HDL VI DI	REMARK	STRUCTURAL PROTEIN TWO	REPEATS OF SPECITIN, ALPHA	HELICAL LINKER REGION, 2 2	STRICT IR AT PROTEIN		ENDOCYTOSIS/EXOCYTOSIS NSEC1: PROTEIN-PROTEIN	COMPLEX, MULTI-SUBUNIT	ENDOCYTOSIS/EXOCYTOSIS	SYNAPTOTAGMIN ASSOCIATED 35	KDA PROTEIN, P35A, THREE HELIX	BUNDLE	ENDOCYTOSIS/EXOCYTOSIS	SYNAPTOTAGMIN ASSOCIATED 35	KDA PROTEIN, P35A, THREE HELIX	ENDOCYTOSIS/EXOCYTOSIS	SYNAPTOTAGMIN ASSOCIATED 35	KDA PROTEIN, P35A, THREE HELIX	BUNDLE
Coumpound	KINASE; CHAIN: NULL;		STAT3B; CHAIN: A; 18-MER DESOXYOLIGONUCLEOTIDE:	CHAIN: B;		APOLIPOPROTEIN E; CHAIN: A;			-	ALPHA SPECTRIN; CHAIN: A,	, c,				SYNTAXIN BINDING PROTEIN 1: CHAIN: A: SYNTAXIN 1A:	CHAIN: B;	SYNTAXIN-1A; CHAIN: A, B, C;				SYNTAXIN-1A; CHAIN: A, B, C;			SYNTAXIN-1A: CHAIN: A B C:			
SEQFOL D score																											
PMF			0.04			0.04				-0.06				300	0.30		0.28				9.0			0.18			_
Verify			20.0			0.20				0.04				000	-0.22		0.11				-0.41			-0.04			
Psi Blast			1.1e-07			1.6e-05				3e-13				0. 1	7.5e-19		4.5e-07				1.5e-08			1e-09			
END			198			126		.,.,		259				900	867		260	,			298			394			,
STAR T AA			36			6				24				60	×0 		118				138		· · · · · · · · · · · · · · · · · · ·	246			
CHAI N ID	•		⋖			A				¥				þ	2		¥				∢			¥			
PDB ID			lbg1			1bz4				1cun				1.4.1	Tue!		lez3				lez3			lez3			
SEQ ID	NO:		1782			1782				1782				7007	78/1		1782				1782			1782			

PDB annotation	MEMBRANE PROTEIN FOUR HELIX BUNDLE, ALPHA HELIX	MEMBRANE PROTEIN FOUR HELIX BUNDLE, ALPHA HELIX	DNA-BINDING HMGA DNA- BINDING HMG-BOX DOMAIN A OF RAT HMG1; 1AAB 8 HMG-BOX 1AAB 20	SIGNALING PROTEIN GUANINE	NUCLEOTIDE- BINDING PROTEIN 1;	GBP, GTP HYDROLYSIS, GDP, GMP, INTERFERON INDITCED DYNAMIN	2 RELATED, LARGE GTPASE	FAMILY, SIGNALING PROTEIN	SIGNALING PROTEIN GBP, GTP	ALLONOLISIS, GDF, GMF,	18 TEM EACH INDOCED, D. INAMINA 2 RELATED. LARGE GTPASE	FAMILY, GMPPNP, GPPNHP.	SERINE/THREONINE PROTEIN	KINASE TRANSFERASE,	SERINE/THREONINE-PROTEIN	KINASE, 2 PROTO-ONCOGENE,	ZINC, ATP-BINDING, PHORBOL-				-		-	SIGNALLING PROTEIN TYPE I RECEPTOR, STNFR1; INCF 8
Coumpound	SSO1 PROTEIN; CHAIN: A;	SSOI PROTEIN; CHAIN: A;	HIGH MOBILITY GROUP PROTEIN; 1AAB 5 CHAIN: NULL; 1AAB 6	INTERFERON-INDUCED	GUANYLATE-BINDING	PROTEIN I; CHAIN: A;	•	Company of the comment of the commen	INTERFERON-INDOCED	DROTTEN 1: CHAIN: A:	TANCIETY IS CHARTE TO		RAF-1; CHAIN: NULL;					DNA-BINDING HIGH	MOBILITY GROUP PROTEIN	FRAGMENT-B (HMGB) (DNA-	BINDING 1HME 3 HMG-BOX	DOMAIN B OF RAT HMG1)	(NMR, 1 STRUCTURE) 1HME 4	TUMOR NECROSIS FACTOR RECEPTOR; INCF 4 CHAIN: A,
SEQFOL D score			,																	,				
PMF score	0.04	0.03	0.03	0.19					40.0				0.03					0.00				,		0.12
Verify score	-0.09	-0.28	-0.24	0.02				5	70.0				-0.40		_			-0.29						0.02
Psi Blast	7.5e-07	le-11	0.00012	4.5e-05				20000	0.00013				0.003					0.0045						0.006
END AA	485	280	763	2333	•			2222	555				8				*****	753	•					141
STAR T AA	283	65	716	7223				2007	157				69					716				····		17
CHAI N ID	Ą	Ą		¥		,			ς,	•														₩.
PDB ID	1fio	1fio	laab	1dg3				156	1				l faq					1hme		-				Incf
SEQ ID No:	1782	1782	1783	1783				1702	1,03				1783					1783				,		1783

PDB annotation	BINDING PROTEIN, CYTOKINE INCF 19	PHOSPHOTRANSFERASE	CALCIUM-BINDING PROTEIN RAT BRAIN PKC-G; CALCIUM-BINDING PROTEIN, PROTEIN KINASE C, PKC,	CALCIUM-BINDING PROTEIN RAT BRAIN PKC-G; CALCIUM-BINDING PROTEIN, PROTEIN KINASE C, PKC, TRANSFEPASE	GENE REGULATION/DNA LEF-1 HMG; LEF1, HMG, TCR-A, TRANSCRIPTION FACTOR, DNA BINDING, DNA 2 BENDING, COMPLEX (HMG DOMAIN/DNA), GENE REGULATION/DNA	CALCIUM-BINDING PROTEIN RAT BRAIN PKC-G; CALCIUM-BINDING PROTEIN, PROTEIN KINASE C, PKC, TRANSFERASE	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING	I NOTEIN
Coumpound	B; INCF 5	PROTEIN KINASE C DELTA TYPE; 1PTQ 4	PROTEIN KINASE C, GAMMA TYPE; CHAIN: NULL;	PROTEIN KINASE C, GAMMA TYPE; CHAIN: NULL;	LYMPHOID ENHANCER- BINDING FACTOR; CHAIN: A; DNA (5'- CHAIN: B; DNA (5'- CHAIN: C;	PROTEIN KINASE C, GAMMA TYPE; CHAIN: NULL;	QGSR ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING SITE: CHAIN: B. C.	DNA-BINDING PROTEIN HUMAN ENHANCER-BINDING PROTEIN MBP-1 MUTANT WITH CYS 11 1BBO 3 REPLACED BY ABU (C11ABU) (NMR, 60 STRUCTURES) 1BBO
SEQFOL D score								
PMF score		0.23	0.31	0.41	0.31	0.01	0.45	-0.13
Verify score		0.02	-0.09	-0.35	-0.13	-0.65	-0.30	0.07
Psi Blast		0.003	0.00075	0.006	7.5e-05	0.0009	3.2e-26	3.2e-12
END AA		50	50	66	763	137	130	232
STAR T AA		21	21	69	716	100	62	178
CHAI N ID					A		4 •	
PDB ID		1 ptq	1tbn	Itbn	2lef	ltbn	la1h	1bbo
SEQ ID NO:		1783	1783	1783	1783	1784	1785	1785

und PDB annotation		OTEIN ER-BINDING IUTANT 3 3 U (C11ABU) URES) IBBO	EK EK	D. E. COMPLEX (ZINC FINGERDNA) ZINC FINGER FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER D)NA)			TEIN ALPHA; COMPLEX (TRANSCRIPTION DING REGULATION/DNA) GABPALPHA; CHAIN: B: GABPBETA!: COMPLEX		
Coumpound	4	DNA-BINDING PROTEIN HUMAN ENHANCER-BINDING PROTEIN MBP-1 MUTANT WITH CYS 11 1BBO 3 REPLACED BY ABU (C11ABU) (NMR, 60 STRUCTURES) 1BBO	DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	ADRI; CHAIN: NULL;	GA BINDING PROTEIN ALPHA; CHAIN: A; GA BINDING PROTEIN BETA I; CHAIN: B;	DNA CHAIN DE	DNA; CHAIN: D, E;
SEQFOL D score									-
PMF		0.04	0.04	0.04	0.05	0.90	0.52		
Verify score		-0.88	-0.42	-0.19	-0.23	-0.01	-0.23		
Psi Blast		1.6e-12	1.6e-42	4.8e-41	3.2e-12	4.8e-18	8e-34	_	
END		113	98	114	114	117	157	_	
STAR T AA		64	15	43	87	62	00	_	
CHAI N ID			၁	၁	Ð		Ф	_	_
PDB ID		1550	Imey	Imey	Imey	2adr	Iawc	_	
SEQ ID NO:		1785	1785	1785	1785	1785	1788	_	

	PDB annotation	TRANSCRIPTION 3 FACTOR	IN ALPHA; COMPLEX (TRANSCRIPTION			(TRANSCRIPTION	REGULATION/DNA), DNA-BINDING,	2 NUCLEAR PROTEIN, ETS DOMAIN,	ANKYRIN REPEATS,	 HIBITOR; TUMOR SUPPRESSOR TUMOR	SUPPRESSOR, CDK4/6 INHIBITOR,	ANKYRIN MOTIF	IT KINASE COMPLEX (KINASE/ANTI-	PLE ONCOGENE) CDK6; P16INK4A,		KINASE, CYCLIN DEPENDENT	KINASE INHIBITORY 2 PROTEIN,	CDK, INK4, CELL CYCLE, MULTIPLE	TUMOR SUPPRESSOR, 3 MTS1,	COMPLEX (KINASE/ANTI-	ONCOGENE) HEADER	H		_	KINASE, CELL CYCLE 2 CONTROL,	ALPHA/BETA, COMPLEX	(INHIBITOR PROTEIN/KINASE)	T KINASE COMPLEX (INHIBITOR	4D; CHAIN: PROTEIN/KINASE) INHIBITOR		KINASE, CELL CYCLE 2 CONTROL,	ALPHA/BETA, COMPLEX	7	
	SECFUL Coumpound D score		GA BINDING PROTEIN ALPHA;	CHAIN: A; GA BINDING	PROTEIN BETA I; CHAIN: B;	DNA; CHAIN: D, E;			~~	P19INK 4D CDK 4/6 INHIBITOR;	CHAIN: NULL;		CYCLIN-DEPENDENT KINASE	6; CHAIN: A; MULTIPLE	TUMOR SUPPRESSOR; CHAIN:	M						CYCLIN-DEPENDENT KINASE	6; CHAIN: A; P19INK4D; CHAIN:	'n	*:			CYCLIN-DEPENDENT KINASE	6; CHAIN: A; P19INK4D; CHAIN:	B;		-		THE RESERVE THE PROPERTY OF THE PARTY OF THE
ŀ	score		0.29							0.19			20.0									0.00			•			0.37						•
	verity		-0.09					-		-0.01			0.14					• •	*****			-0.17						0.01	•					·
	rsi blast		4.8e-29							8e-27			6.4e-17			•		•	-			6.4e-26				•		1.3e-23				1 4 40		_
20.00	AA AA		125			4. m. k				160	_		 260								\forall	99						83					1	-20
8	TAA		3							21			443									.75	M Lu a an			-		ଜ	-			_		_
11,000	NED OF		м				- Marie de						<u></u>							•		m						<u>—</u>						<
ממת	E C		lawc							1bd8			1bi7									I plx		_				1b[x				•		0
000	ğ a ğ		1788		_			•		1788			1788				Radio Pet 6					1788		- ",			1	1788				*****	90.5	788

PDB annotation	INK4C; CELL CYCLE INHIBITOR, P18INK4C, TUMOR, SUPPRESSOR, CYCLIN- 2 DEPENDENT KINASE, HORMONE/GROWTH FACTOR	SIGNALING PROTEIN HELIX-TURN- HELIX, ANKYRIN REPEAT	CELL CYCLE INHIBITOR P18- INK4C(INK6); CELL CYCLE INHIBITOR, P18-INK4C(INK6), ANKYRIN REPEAT, 2 CDK 4/6 INHIBITOR	CELL CYCLE INHIBITOR P18- INK4C(INK6); CELL CYCLE INHIBITOR, P18-INK4C(INK6), ANKYRIN REPEAT, 2 CDK 4/6 INHIBITOR	ANK-REPEAT MYOTROPHIN, ACETYLATION, NMR, ANK-REPEAT	SIGNALING PROTEIN RUB1, UBIQUITIN-LIKE PROTEIN, ARABIDOPSIS, SIGNALING PROTEIN	DE NOVO PROTEIN PROTEIN DESIGN, HYDROPHOBIC CORE, PACKING, ROTAMERS, ROC, 2 UBIQUITIN, DE NOVO PROTEIN, UBIQUITIN	SIGNALING PROTEIN NEDD8; NEDD8, NEDD-8, UBIQUITIN-LIKE, PROTEOLYSIS, SIGNALING 2 PROTEIN	
Coumpound	6 INHIBITOR; CHAIN: A;	CYCLIN-DEPENDENT KINASE 4 INHIBITOR B; CHAIN: A;	CYCLIN-DEPENDENT KINASE 6 INHIBITOR; CHAIN: A, B;	CYCLIN-DEPENDENT KINASE 6 INHIBITOR; CHAIN: A, B;	MYOTROPHIN; CHAIN: NULL	UBIQUITIN-LIKE PROTEIN 7, RUB1; CHAIN: A;	1D8 UBIQUITIN; CHAIN: A;	UBIQUITIN-LIKE PROTEIN NEDD8; CHAIN: A, B, C, D;	UBIQUITIN TETRAUBIQUITIN 1TBE 3
SEQFOL D score									
PMF score		90.0	0.10	0.37	0.01	0.92	0.76	0.75	0.94
Verify score		0.14	-0.12	0.01	0.14	0.17	0.02	0.22	0.48
Psi Blast		1.6e-17	1.3e-25	3.2e-24	1.6e-20	1.4e-20	1.6e-27	6.46-20	3.2e-27
END		267	191	129	127	194	196	195	193
STAR T AA		443	18	·	19	124	124	124	124
CHAI N ID		¥	٧	¥.		Ą	Ą	∢	В
PDB ID		149s	1716	1ihb	1myo	1bt0	1c3t	lndd	1tbe
SEQ ID NO:		1788	1788	1788	1788	1791	1791	1791	1791

WO 02/070539 PCT/US02/05095

PDB annotation		UBIQUITIN UBIQUITIN, DESIGNED CORE MUTANT	TRANSCRIPTION TUMOR SUPPRESSOR, CANCER, UBIQUITIN, BETA SANDWICH, 2 TRANSCRIPTION, TRANSCRIPTION,	MATRIX PROTEIN M-PMV MA MATRIX PROTEIN, CORE PROTEIN, POLYPROTEIN, MYRISTYLATION	MATRIX PROTEIN M-PMV MA MATRIX PROTEIN, CORE PROTEIN, POLYPROTEIN, MYRISTYLATION	ENDOCYTOSIS/EXOCYTOSIS NSECI; PROTEIN-PROTEIN COMPLEX, MULTI-SUBUNIT	ENDOCYTOSIS/EXOCYTOSIS NSECI; PROTEINPPRETEIN COMPLEX, MULTI-SUBUNIT		MUSCLE PROTEIN CTNC; CARDIAC, MUSCLE PROTEIN, REGULATORY, CALCIUM BINDING	MUSCLE PROTEIN CTNC; CARDIAC, MUSCLE PROTEIN, REGULATORY,	CALCIUM BINDING	CALMODULIN CERIUM TRIC- DOMAIN, RESIDUES 1 - 75: CERIUM-
Coumpound	CHROMOSOMAL PROTEIN UBIQUITIN 10BI 3	UBIQUITIN CORE MUTANT 107; CHAIN: A;	ELONGIN B; CHAIN: A, D, G, J; ELONGIN C; CHAIN: B, E, H, K; VHL; CHAIN: C, F, I, L;	M-PMV MATRIX PROTEIN; CHAIN: NULL;	M-PMV MATRIX PROTEIN; CHAIN: NULL;	SYNTAXIN BINDING PROTEIN I; CHAIN: A; SYNTAXIN 1A; CHAIN: B;	SYNTAXIN BINDING PROTEIN 1; CHAIN: A; SYNTAXIN 1A; CHAIN: B;		TROPONIN C; CHAIN: NULL;	TROPONIN C; CHAIN: NULL;	CAT MODITI IN: CHAIN: NI II I	
SEQFOL D score					69.49	·			57.92			
PMF score	0.66	0.55	0.15	0.64		0.00	0.00			0.25	-0.01	
Verify	0.19	0.39	-0.54	-0.22		-0.04	-0.04		· ·	0:30	0.12	
Psi Blast	4.8e-29	3.2e-28	6.4e-05	3.2e-36	3.2e-36	0.0075	0.0075		6.4e-36	6.4e-36	4.8e-16	
END	961	196	181	92	92	227	235		382	379	309	
STAR TAA	124	124	124			157	165		225	241	241	
CEAI N ID		Ą	Ą			м	æ	•				
PDB ID	Iubi	lud7	1vcb	Ibax	1bax	1dn1	Idn1		laj4	1aj4	lak8	
SEQ D NO:	1791	16/1	1791	1792	1792	1794	1795		1799	1799	1799	

PDB T	CHAI	STAR	END	Psi Blast	Verify	PMF	SEQFOL	Coumpound	PDB annotation
		-			score	score	D score		
J									LOADED, CALCIUM-BINDING PROTEIN
lap4		241	314	1.4e-12	0.50	-0.01		CARDIAC N-TROPONIN C; CHAIN: NULL;	CALCIUM-BINDING CNTNC; CALCIUM-BINDING, REGULATION, TROPONIN C, CARDIAC MUSCLE 2
1	m	233	391	4.8e-42			69.73	SERINE/THREONINE PHOSPHATASE 2B; CHAIN: A,	HYDROLASE CALCINEURIN; HYDROLASE, PHOSPHATASE,
1	В	240	378	4.8e-42	0.46	0.68		ESERINE/THREONINE PHOSPHATASE 2B; CHAIN: A, B:	IMMONOSOFRESSION HYDROLASE CALCINEURIN; HYDROLASE, PHOSPHATASE NAMI NIOSI IPPOPERIOTA
	• 4	202	345	3.2e-11	-0.02	0.19		NEUROCALCIN DELTA; CHAIN: A, B;	CALCIUM-BINDING CALCIUM-BINDING, MYRISTOYLATION, NEURONAL SPECIFIC GUANYLATE CYCI ASE ACTIVATOR
	∢	224	385	6.4e-36	0.64	0.83		NEUROCALCIN DELTA; CHAIN: A, B;	CALCTUM-BINDING CALCTUM- BINDING, MYRISTOYLATION, NEURONAL SPECIFIC GUANYLATE 2 CYCLASE ACTIVATOR
	¥	224	390	6.4e-36			59.92	NEUROCALCIN DELTA; CHAIN: A, B;	CALCIUM-BINDING CALCIUM- BINDING, MYRISTOYLATION, NEURONAL SPECIFIC GUANYLATE 2 CYCLASE ACTIVATOR
lcdm	₹.	241	378	3.2e-42	0.25	0.18		CALCIUM-BINDING PROTEIN CALMODULIN COMPLEXED WITH CALMODULIN-BINDING DOMAIN OF ICDM 3 CALMODULIN-DEPENDENT PROTEIN KINASE II ICDM 4	
		241	378	3.2e-47	0.05	0.21		CALCIUM-BINDING PROTEIN CALMODULIN (VERTEBRATE) 1CLL 3	
		241	380	3.2e-47			59.19	CALCIUM-BINDING PROTEIN	

			, iii	Ä	٠			ĽĽ,	~ ×	~ ×	Z	ZIZ	ST	2
PDB annotation			CALCIUM-BINDING PROTEIN CALMODULIN APO TR2C-DOMAIN; ICMF 9	CALCIUM-BINDING PROTEIN CALMODULIN APO TR2C-DOMAIN;	BLOOD CLOTTING HELICAL, EF- HAND, BLOOD CLOTTING	STRUCTURAL PROTEIN HELIX- TURN-HELIX	STRUCTURAL PROTEIN HELIX- TURN-HELIX	METAL TRANSPORT CALMODULIN, HIGH RESOLUTION, DISORDER	TRANSPORT PROTEIN CALCIUM BINDING, EF HAND, FOUR-HELIX BUNDLE	TRANSPORT PROTEIN CALCIUM BINDING, EF HAND, FOUR-HELIX BUNDI.E	CONTRACTILE PROTEIN TROPONIN C-TROPONIN I INTERACTION, CARDIAC, MUSCLE PROTEIN, 2 CALCHIM BINDING PROTEIN	CONTRACTILE PROTEIN TROPONIN C-TROPONIN I INTERACTION, CARDIAC, MUSCLE PROTEIN, 2 CALCHM RINDING PROTEIN	METAL BINDING PROTEIN YEAST	LYASE GCAP-2; EF-HAND, CALCIUM-BINDING PROTEIN,
			CALCIU CALMO	CALCIC	HAN	STR.	STR	MET	BINI	TRANSPO BINDING BUNDILE	SE SE	CAR C	MET	CALC
Coumpound	·	CALMODULIN (VERTEBRATE)	CALMODULIN (VERTEBRATE); ICMF 6 CHAIN: NULL; 1CMF 7	CALMODULIN (VERTEBRATE); ICMF 6 CHAIN: NULL; 1CMF 7	APO CIB; CHAIN: A	CARDIAC TROPONIN C; CHAIN: A;	CARDIAC TROPONIN C; CHAIN: A;	CALMODULIN; CHAIN: A;	CALMODULIN; CHAIN: A;	CALMODULIN; CHAIN: A;	TROPONIN C; CHAIN: A;	TROPONIN C; CHAIN: A;	CALCIUM-BINDING PROTEIN NCS-1: CHAIN: A:	GUANYLATE CYCLASE ACTIVATING PROTEIN 2;
SEQFOL	D score	-												
PMIF	score		0.13	-0.06	09.0	0.07	69.0	0.12	0.60	0.16	0.21	0.18	0.03	0.99
Verify	score		0.73	0.43	0.01	90.0	0.16	0.13	0.40	0.44	0.25	0.10	0.18	0.46
Psi Blast	-		4.8e-11	1.6e-25	3.2e-20	1.4e-12	8e-36	1.3e-44	8e-11	3.2e-24	9.6e-10	1.3e-19	3.2e-15	1.6e-29
END	AA		309	378	388	306	379	378	309	378	306	379	341	392
STAR	I WW		242	310	241	183	241	241	247	316	238	313	221	241
CHA1					Ą	∢	∢	¥.	∢	4	Ą	Ą	A	Ą
PDB	3		1cmf	lcmf	1dgv	1 4 £1	I d El	lexr	Ē	1771	1fi5	1fi5	1fpw	1jba
SEQ	NO:		1799	1799	1799	1799	1799	1799	1799	1799	1799	1799	1799	1799

No.

PDB annotation	GUANYLYL CYCLASE 2 REGULATION	CALCIUM-REGULATED MUSCLE	CONTRACTION MUSCLE CONTRACTION, CALCIUM-	BINDING, TROPONIN, E-F HAND, 2	REGULATORY DOMAIN. CALCIUM-	REGULATED 3 MUSCLE CONTRACTION	CALCIUM-REGULATED MUSCLE	CONTRACTION MUSCLE	BINDING, TROPONIN, E-F HAND, 2	OPEN CONFORMATION	REGULATORY DOMAIN, CALCIUM-	REGULATED 3 MUSCLE CONTRACTION	CALCIUM-BINDING PROTEIN EF-	CALCITIMERINDING PROTEIN FE.	HAND ITNX 14										
Coumpound	CHAIN: A;	TROPONIN C; CHAIN: NULL;					TROPONIN C; CHAIN: NULL;						TROPONIN C; 1TNX 4 CHAIN:	TROPONIN C. 1TNX 4 CHAIN:	NULL; ITNX 5	CONTRACTILE SYSTEM PROTEIN TROPONIN C 170P 3	CONTRACTILE SYSTEM	PROTEIN TROPONIN C 170P 3	CALCIUM BINDING PROTEIN	CALMODULIN (/TR=2=C\$	PRACIMENT COMPRISING	THE WITHOUT WAS INCOME.	THE INTACT MOLECULE) TINC	CALCIUM BINDING PROTEIN	CALMODULIN (/TR=2=C\$
SEQFOL D score				-			63.35		-				69.19			64.51									
PMF		0.48												0.05			0.41		-0.05					-0.09	
Verify score		0.10												-0.22			0.02		0.28					0.03	
Psi Blast		3.2e-37					3.2e-37			•			4.8e-36	4.8e-36		3.2e-38	3.2e-38		6.4e-11		•			1.1e-24	
END AA		378					379						378	378		382	378		306					378	
STAR T AA		232	444				233						233	236		227	236		242					314	
CHAI N ID																			¥					∢	
PDB ID		ltcf					1tcf						T X X	ltmx		Itop	1top		1112					Itro	
SEQ ON NO:		1799					1799						1799	1799		1799	1799		1799					1799	

		Ğ. Ğ.	G, 2,	G, 2,		Z, Z,	ÜŽŽ		
PDB annotation		CALMODULIN, CALCIUM BINDING, HELIX-LOOP-HELIX, SIGNALLING, 2 COMPLEX(CALCIUM-BINDING PROTEIN/PEPTIDE)	CALMODULIN, CALCIUM BINDING, HELIX-LOOP-HELIX, SIGNALLING, 2 COMPLEX(CALCIUM-BINDING PROTEIN/PEPTIDE)	CALMODULIN, CALCIUM BINDING, HELIX-LOOP-HELIX, SIGNALLING, 2 COMPLEX(CALCIUM-BINDING PROTEIN/PEPTIDE)	MUSCLE PROTEIN MYOSIN, CALCIUM BINDING PROTEIN, MUSCLE PROTEIN	CALCIUM-BINDERG PROTEIN CTNC; CARDIAC, MUSCLE, REGULATORY, CALCIUM-BINDING PROTEIN	CALCIUM-BINDING PROTEIN CTNC; CARDIAC, MUSCLE, REGULATORY, CALCIUM-BINDING PROTEIN	COMPLEX (ZINC FINGER/DNA), COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN	COMPLEX (ZINC FINGER/DNA), COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING
Coumpound	FRAGMENT COMPRISING RESIDUES 78 - 148 1TRC 3 OF THE INTACT MOLECULE) 1TRC	CALMODULIN; CHAIN: A; RS20; CHAIN: B;	CALMODULIN; CHAIN: A; RS20; CHAIN: B;	CALMODULIN; CHAIN: A; RS20; CHAIN: B;	SCALLOP MYOSIN; CHAIN: A, B, C;	TROPONIN C; CHAIN: NULL;	TROPONIN C; CHAIN; NULL;	QGSR ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C.	QGSR ZINC FINGER PEPTIDE; ' CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING SITE: CHAIN: B. C.
SEQFOL D score			56.76						
PMF		0.07		0.33	0.04	0.13	0.12	0.35	86.0
Verify score		-0.21		0.12	0.23	0.36	0.19	0.03	0.03
Psi Blast		1.6e-14	3.26-46	3.26-46	1.4e-20	9.6e-10	1.3e-19	1.6e-12	4.8e-19
END AA		309	381	378	382	306	379	210	238
STAR T AA		180	239	241	241	238	313	120	158
CHAI N ID		Ą	Ą	4	ပ	•		Ą	¥
PDB ID		Ivrk	lvrk	lvrk	1wdc	3ctn	3cm	laih	laih
SEQ ID NO:		1799	1799	1799	1799	1799	1799	1801	1801

o,	PDB	CHAI	STAR	END	Psi Blast	Verify	PMF	SEQFOL	Coumpound	PDB annotation
Ξÿ	a	N ID	TAA	AA		auoss	score	D score		
1801	lalh	¥	214	296	4.5e-37			84.50	QGSR ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OI IGONIC! FOTIDE BINDING	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA, BINDING
									SITE; CHAIN: B, C.	PROTEIN
1801	lalh	∢.	270	377	1.1e-29	0.23	1,00	-1	QGSR ZINC FINGER PEPTIDE;	COMPLEX (ZINC'FINGER/DNA)
		•			•	-		-	CHAIN: A; DUPLEX	COMPLEX (ZINC FINGER/DNA),
									OLIGONUCLEOTIDE BINDING	ZINC FINGER, DNA-BINDING
1801	1914	_	330	2777	0.62.20	2.0	;;		SILE, CHAIN: B, C;	rkojejiv
	14111	¢	0/7	//	27-30.6	01:0	0.41	:	OGSK ZINC FINGER PEPTIDE; CHANE, A. DEBE EV	COMPLEX (ZINC FINGER/DNA)
									OF IGORATOR EOTERS BINESIS	COMPLETA (CHAC FINGERIDINA),
									SITE; CHAIN: B. C.	PROTEIN
1801	lalh	∢	298	404	1.6e-19	0.22	0.57		QGSR ZINC FINGER PEPTIDE;	COMPLEX (ZINC FINGER/DNA)
									CHAIN: A; DUPLEX	COMPLEX (ZINC FINGER/DNA).
									OLIGONUCLEOTIDE BINDING	ZINC FINGER, DNA-BINDING
1	,								SITE; CHAIN: B, C;	PROTEIN
1801	lalh	₹	298	454	3e-19	0.11	0.66		QGSR ZINC FINGER PEPTIDE;	COMPLEX (ZINC FINGER/DNA)
									CHAIN: A; DUPLEX	COMPLEX (ZINC FINGER/DNA),
									OLIGONUCLEOTIDE BINDING	ZINC FINGER, DNA-BINDING
				,					SITE; CHAIN: B, C;	PROTEIN
1087	la!h	<	353	461	3e-21	0.07	0.78		QGSR ZINC FINGER PEPTIDE;	COMPLEX (ZINC FINGER/DNA)
									CHAIN: A; DUPLEX	COMPLEX (ZINC FINGER/DNA),
									OLIGONUCLEOTIDE BINDING	ZINC FINGER, DNA-BINDING
1801	1811	4	382	481	30-06	0 17	0.15		OGSO TRICERICED DEPARTE	PROLEIN
:		1	1	:	77-77-7	7.5	3		COAR ZINC FINGER FEFTIDE;	COMPLEX (ZINC FINGER/DDA)
					_				Circus, A; DOFLEA	COMPLEX (ZINC FINGERODNA),
									OUIGONUCLEOTIDE BINDING	ZINC FINGER, DNA-BINDING
1									SITE; CHAIN: B, C;	PROTEIN
108	ia n	∢	429	25 25 25	8e-30	0.45	8.		QGSR ZINC FINGER PEPTIDE;	COMPLEX (ZINC FINGER/DNA)
									CHAIN: A; DUPLEX	COMPLEX (ZINC FINGER/DNA),
_,									OLIGONUCLEOTIDE BINDING	ZINC FINGER, DNA-BINDING
7									SITE; CHAIN: B, C;	PROTEIN
1081	laih	∢	429	510	9e-31	0.54	1.00		QGSR ZINC FINGER PEPTIDE;	COMPLEX (ZINC FINGER/DNA)
7									CHAIN: A; DUPLEX	COMPLEX (ZINC FINGER/DNA),

5z	CHAI	STAR	END	Psi Blast	Verify	PMF	SEQFOL D score	Coumpound	PDB annotation
		*						OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	ZINC FINGER, DNA-BINDING PROTEIN
	₽.	457	537	1.1e-30	-0.09	0.1 0.1	1 27	QGSR ZINC FINGER PEPTIDE; CHAIN: A: DUPLEX	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA).
								OLIGONUCLEOTIDE BINDING SITE: CHAIN: B. C.	ZINC FINGER, DNA-BINDING PROTFIN
	A	485	565	7.5e-34	0.28	1.00		QGSR ZINC FINGER PEPTIDE;	COMPLEX (ZINC FINGER/DNA)
		•• •		-		*		OLIGONUCLEOTIDE BINDING	COMPLEX (ZINC FINGER DNA), ZINC FINGER, DNA-BINDING
								SITE; CHAIN: B, C;	PROTEIN
***	ပ	119	210	8e-30	0.10	0.36		DNA; CHAIN: A, B, D, E;	COMPLEX (ZINC FINGER/DNA) ZINC
								CONSENSUS ZINC FINGER	FINGER, PROTEIN-DNA NITERACTION PROTEIN DESIGN 2
									CRYSTAL STRUCTURE. COMPLEX
									(ZINC FINGER/DNA)
	ပ	157	238	1.4e-37	0.42	1.00		DNA; CHAIN: A, B, D, E;	COMPLEX (ZINC FINGER/DNA) ZINC
		×						CONSENSUS ZINC FINGER	FINGER, PROTEIN-DNA
_								PROTEIN; CHAIN: C, F, G;	INTERACTION, PROTEIN DESIGN, 2
									CRYSTAL STRUCTURE, COMPLEX
-			,	,					(ZINC FINGER/DNA)
	ບ	581	992	3.2e-47	0.55	0		DNA; CHAIN: A, B, D, E;	COMPLEX (ZINC FINGER/DNA) ZINC
								CONSENSUS ZINC FINGER	FINGER, PROTEIN-DNA
			·					PROTEIN; CHAIN: C, F, G;	INTERACTION, PROTEIN DESIGN, 2
									CRYSTAL STRUCTURE, COMPLEX
	c	0,00	č	0,000	0.00	,			(ZINC FINGER/DNA)
	٠	512	\$	3.2e-48	0.35	00.1		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA
								PROTEIN; CHAIN; C. F. G.	INTERACTION, PROTEIN DESIGN, 2
		·							CRYSTAL STRUCTURE, COMPLEX
									(ZINC FINGER/DNA)
	Ų	241	322	4.8e-49	0.56	1.00		DNA; CHAIN: A, B, D, E;	COMPLEX (ZINC FINGER/DNA) ZINC
								CONSENSUS ZINC FINGER	FINGER, PROTEIN-DNA
								PROTEIN; CHAIN: C, F, G;	INTERACTION, PROTEIN DESIGN, 2
									CRYSTAL STRUCTURE, COMPLEX

SEQ	PDB	CHAI	STAR	END	Psi Blast	Verify	PMF	SEQFOL	Coumpound	PDB annotation
ZÖ.	9		TAA	AA		score	score	D score		
;	,									(ZINC FINGER/DNA)
1801	Imey	ن ن	24	323	4.8e-49			101.14	DNA; CHAIN: A, B, D, E;	COMPLEX (ZINC FINGER/DNA) ZINC
									CONSENSUS ZINC FINGER	FINGER, PROTEIN-DNA
									PROTEIN; CHAIN: C, F, G;	INTERACTION, PROTEIN DESIGN, 2
	,				-					CRYSTAL STRUCTURE, COMPLEX
. 66		ļ								(ZINC FINGER/DNA)
1901	ımey	د	503	377	4.8e-40	-0.06	0.51		DNA; CHAIN: A, B, D, E;	COMPLEX (ZINC FINGER/DNA) ZINC
									CONSENSUS ZINC FINGER	FINGER, PROTEIN-DNA
									PROTEIN; CHAIN: C, F, G;	INTERACTION, PROTEIN DESIGN, 2
										CRYSTAL STRUCTURE, COMPLEX
	,	,								(ZINC FINGER/DNA)
1081	Imey	သ	237	453	1.1e-20	0.01	-0.17		DNA; CHAIN: A, B, D, E;	COMPLEX (ZINC FINGER/DNA) ZINC
									CONSENSUS ZINC FINGER	FINGER, PROTEIN-DNA
									PROTEIN; CHAIN: C, F, G;	INTERACTION, PROTEIN DESIGN, 2
										CRYSTAL STRUCTURE, COMPLEX
.00	,									(ZINC FINGER/DNA)
1801	Imey	၁	353	481	1.3e-22	0.42	0.70		DNA; CHAIN: A, B, D, E;	COMPLEX (ZINC FINGER/DNA) ZINC
						•			CONSENSUS ZINC FINGER	FINGER, PROTEIN-DNA
									PROTEIN; CHAIN; C, F, G;	INTERACTION, PROTEIN DESIGN, 2
					-					CRYSTAL STRUCTURE, COMPLEX
.00	,	,								(ZINC FINGER/DNA)
1001	Illey	ر	725	453	8e-41	0.41	0.24		DNA; CHAIN: A, B, D, E;	COMPLEX (ZINC FINGER/DNA) ZINC
									CONSENSUS ZINC FINGER	FINGER, PROTEIN-DNA
									PROTEIN; CHAIN: C, F, G;	INTERACTION, PROTEIN DESIGN, 2
										CRYSTAL STRUCTURE, COMPLEX
1001	1	C	100	1	,					(ZINC FINGER/DNA)
1001	IIIEy		381	4 2 1	3.2e-45	0.26	0.07		DNA; CHAIN: A, B, D, E;	COMPLEX (ZINC FINGER/DNA) ZINC
	****		·		-				CONSENSUS ZINC FINGER	FINGER, PROTEIN-DNA
									PROTEIN; CHAIN: C, F, G;	INTERACTION, PROPERTOESIGN, 2
		•						•	,	CRYSTAL STRUCTURE, COMPLEX
1001			9	\dagger	9.					(ZINC FINGER/DNA)
100	riney	ر	470	<u></u>	1.be-49	16.0	9:-		DNA; CHAIN: A, B, D, E;	COMPLEX (ZINC FINGER/DNA) ZINC
					***************************************		,		PROTEIN: CHAIN: OF A	FINGER, FROIEIN-DINA
									Trottom, cumin. c, 1, C,	INTERCACION, I NOTEDIN DESIGN, 2

r ds andeallon	CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)	60	C. F. G: INTERACTION PROTEIN DESIGN 2	 		C FINGER FINGER, PROTEIN-DNA		(ZINC FINGER/DNA)	R IIIA;		GENE; NMR, TFIIIA, PROTEIN, DNA,	TRANSCRIPTION FACTOR, 58 RNA 2	GENE, DNA BINDING PROTEIN,	CINC FINGER, COMPLEX 3	(IKANSCRIPTION		RECOLATION/DIA)		D; 5S GENE;	D; 5S GENE;	D; 5S GENE;	D; 5S GENE;	D; SS GENE;	D; SS GENE;	ńî	ái ái	ńî ńî	ii iii	rii rii
Countyoung		DNA; CHAIN: A, B, D, E;	PROTEIN: CHAIN: C. F. G.		DNA; CHAIN: A, B, D, E;	PROTEIN: CHAIN: C F C:	()		TRANSCRIPTION FACTOR IIIA;	CHAIN: A; 58 RNA GENE;	CHAIN: E, F;							TFIIIA; CHAIN: A, D; 5S	TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE;	TFIIIA; CHAIN: A, D; RIBOSOMAL RNA GI CHAIN: B, C, E, F;	TFIIIA; CHAIN: A, D; RIBOSOMAL RNA GI CHAIN: B, C, E, F;	TFIIIA; CHAIN: A, D; RIBOSOMAL RNA GI CHAIN: B, C, E, F;	TFIIIA; CHAIN: A, D; RIBOSOMAL RNA Gi CHAIN: B, C, E, F;	TFIIIA; CHAIN: A, D; RIBOSOMAL RNA Gi CHAIN: B, C, E, F;	TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GEN CHAIN: B, C, E, F; TFIIIA; CHAIN: A, D; 5S	TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F; TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE;	TFIIIA; CHAIN: A, D; RIBOSOMAL RNA Gi CHAIN: B, C, E, F; TFIIIA; CHAIN: A, D; RIBOSOMAL RNA GI CHAIN: B, C, E, F;	TFIIIA; CHAIN: A, D; RIBOSOMAL RNA Gi CHAIN: B, C, E, F; TFIIIA; CHAIN: A, D; RIBOSOMAL RNA GI CHAIN: B, C, E, F;	TFIIIA; CHAIN: A, D; RIBOSOMAL RNA Gi CHAIN: B, C, E, F; TFIIIA; CHAIN: A, D; RIBOSOMAL RNA Gi CHAIN: B, C, E, F;
D scare				 		-										_								11 in	114.65	114.65	114.65	114.65	114.65
score		0.99			8.				-0.01									0.22	0.22	0.22	0.22	0.22	0.22	0.22	0.22	0.22	0.22	0.22	0.22
score		-0.03			0.25				0.23									0.08	0.08	0.08	0.08	0.08	0.08	0.08	0.08	80.00	80.00	80.00	80.00
I St Diast		1.6e-49	4		1.6e-49				6.4e-17	•			,					1.4e-22	1.4e-22	1.4e-22	1.4e-22	1.4e-22	1.4e-22	1.4e-22	1.4e-22 3e-61	1.4e-22 3e-61	1.4e-22 3e-61	1.4e-22 3e-61	1.4e-22 3e-61
A F		537			565				481									247	247	247	247	247	247	247	247	325	325	325	325
TAA		456			484				382			-						112	112	112	112	112	112	112	112	112	112	112	112
A N		၁			ပ				Ą	•								Ą	Ą	₹	4	₹	4	¥.	4 4	4 4	4 4	₹	₹
e		Imey			Imey				1463									1466	1416	1466	11466	146	146	146	1146	148 148	1116	1146	146
g e g		1801			1801				1801									1801	1801	1801	1801	1801	1801	1801	1801	1801	1801	1801	1801

PDB annotation	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN	COMPLEX (TRANSCRIPTION REGULATIONDNA) COMPLEX (TRANSCRPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN	COMPLEX (TRANSCRIPTION REGULATIONDNA) COMPLEX (TRANSCRIPTION REGULATIONDNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER, PROTEIN	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC
Coumpound	TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	TFIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	TFIIIA: CHAIN: A, D; SS RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	TFIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F,
SEQFOL D score					
PMF score	0.99	1.00	0.24	0.28	0.99
Verify score	0.37	0.15	0.04	-0.15	0,23
Psi Blast	9.66-31	1.4e-35	1.36-25	1.3e-34	1.6e-35
END AA	303	324	495	547	565
STAR T AA	158	186	298	382	429
CHAI N ID	Ф	¥	4	∢	Ą
PDB ID	1466	1476	1476	1tf6	146
SEQ IB NO:	1801	1801	1801	1801	1801

Ind C 157 266 68-45 1.00 VYI; CHAIN: C, ADBNO, COMPLEX (TRANSCRIPTION INTIAL CONFILE)	۳. ا	PDB ID	CHAI N ID	STAR T AA	END AA	Psi Blast	Verify score	PMF	SEQFOL D score	Coumpound	PDB annotation
C 157 266 6e-43 0.25 1.00 ASSOCIATED VIRUS PS INITIATOR BLEMENT DNA; CHAIN: C, ADENO-CHAIN: C,		+									FINGER PROTEIN
C 159 267 7.5e-48 92.90 YY1; CHAIN: A, B; CHAIN: A, B; CHAIN: A, B; CHAIN: A, B; CHAIN: C, ADENO-ASSOCIATED VRUS P5 CHAIN: A, B; CHAIN: C, ADENO-ASSOCIATED VRUS P5 CHAIN: C, ADENO-ASSOCIATED VIRUS P5 CHAIN: C, ADENO-C CASSOCIATED VIRUS P5 CHAIN: C, ADENO-C CASSOCIATE	. ~	· · · · · · · · · · · · · · · · · · ·	C)	157	266	6e-43	0.25	00.1		YYI; CHAIN: C; ADENO. ASSOCIATED VIRUS P5	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1:
C 159 267 7.5e-48 92.90 YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B; CHAIN: A, B; CHAIN: C, ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: C, ADENO-CHAIN: A, B; CHAIN: A, B; CHAIN: A, B; CHAIN: C, ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B; CHAIN: C, ADENO-CHAIN: C, ADENO-C										INITIATOR ELEMENT DNA; CHAIN: A. B:	TRANSCRIPTION INITIATION, INITIATOR FILEMENT VY1 ZINC 2
C 159 267 7.5e-48 92.90 YY1; CHAIN: C, ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B; CHAIN: C, ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B; CHAIN: C, ADENO-C ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B; CHAIN: C, ADENO-C ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B; CHAIN: C, ADENO-C ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B; CHAIN: C, ADENO-C ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B; CHAIN: C, ADENO-C ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: C, ADENO-C ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: C, ADENO-C ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B; CHAIN: C, ADENO-C ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B; CHAIN: C, ADENO-C ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B; CHAIN: C, ADENO-C ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B; CHAIN: C, ADENO-C ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B; CHAIN: C, ADENO-C ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: C, ADENO-C ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B; CHAIN: C, ADENO-C ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B; CHAIN: C, ADENO-C ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: C, ADENO-C ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: C, ADENO-C ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: C, ADENO-C ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; C, ADENO-C ASSOCIATED V											FINGER PROTEIN, DNA-PROTEIN RECOGNITION 3 COMPI PX
C 159 267 7.5e-48 92.90 YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B; INITIATOR ELEMENT DNA; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: C, ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: C, ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: C, ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B; INITIATOR ELEMENT DNA; CHAIN: A, B; INITIATOR ELEMENT DNA; CHAIN: C, ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CANDA-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CANDA-ASSOCI	-										(TRANSCRIPTION REGULATION/DNA)
C 186 294 7.5e-48 0.35 1.00 YY1; CHAIN: C; ADENO- C 217 322 7.5e-51 0.15 1.00 YY1; CHAIN: C; ADENO- ASSOCIATED VIRUS P5 NITIATOR ELEMENT DNA; CHAIN: C, ADENO- ASSOCIATED VIRUS P5 NITIATOR ELEMENT DNA; CHAIN: C, ADENO- ASSOCIATED VIRUS P5 NITIATOR ELEMENT DNA; CHAIN: C, ADENO- C 221 322 1.6e-32 0.17 1.00 YY1; CHAIN: C, ADENO-	=	_	0	159	267	7.5e-48			92.90	YY1; CHAIN: C; ADENO-	COMPLEX (TRANSCRIPTION
C 186 294 7.5e-48 0.35 1.00 YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR BLEMENT DNA; CHAIN: A, B; CHAIN: A, B; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR BLEMENT DNA; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR BLEMENT DNA; CHAIN: A, B; CHAIN: C, ADENO-ASSOCIATED VIRUS P5 INITIATOR BLEMENT DNA; CANDA DNA; C										ASSOCIATED VIRUS P5 NITIATOR RI RAENT DNA:	REGULATION/DNA) YING-YANG 1;
C 186 294 7.5e-48 0.35 1.00 YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B; CHAIN: A, B; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B; CHAIN: C, ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CALARIA			******							CHAIN: A, B;	INITIATOR ELEMENT, YY1, ZINC 2
C 186 294 7.56-48 0.35 1.00 YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B; CHAIN: C; ADENO-CHAIN: C, ADENO-CHAIN: C, ADENO-CHAIN: C; ADENO-CHAIN: C, ADENO-CH											FINGER PROTEIN, DNA-PROTEIN
C 186 294 7.5e-48 0.35 1.00 YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B; CHAIN: C, ADENO-C 221 322 1.6e-32 0.17 1.00 YY1; CHAIN: C; ADENO-YY1; CHAIN: C; ADENO-		-				•			•		RECOGNITION, 3 COMPLEX
C 186 294 7.5e-48 0.35 1.00 YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B; CHAIN: C, ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: C, ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B; CHAIN: A, B; CHAIN: C, ADENO-C 221 322 1.6e-32 0.17 1.00 YY1; CHAIN: C, ADENO-	- 1										(Individual Individual)
C 217 322 7.5e-51 0.15 1.00 YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: C, ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B; CHAIN: A, B; CHAIN: C, ADENO-C 221 322 1.6e-32 0.17 1.00 YY1; CHAIN: C, ADENO-C 221 322 1.6e-32 0.17 1.00 YY1; CHAIN: C, ADENO-C 221 322 1.6e-32 0.17 1.00 YY1; CHAIN: C, ADENO-C 221 322 1.6e-32 0.17 1.00 YY1; CHAIN: C, ADENO-C 221 322 1.6e-32 0.17 1.00 YY1; CHAIN: C, ADENO-C 221 322 1.6e-32 0.17 1.00 YY1; CHAIN: C, ADENO-C 221 322 1.6e-32 0.17 1.00 YY1; CHAIN: C, ADENO-C 221 322 1.6e-32 0.17 1.00 YY1; CHAIN: C, ADENO-C 221 322 1.6e-32 0.17 1.00 YY1; CHAIN: C, ADENO-C 221 322 1.6e-32 0.17 1.00 YY1; CHAIN: C, ADENO-C 221 322 1.6e-32 0.17 1.00 YY1; CHAIN: C, ADENO-C 221 322 1.6e-32 0.17 1.00 YY1; CHAIN: C, ADENO-C 221 322 1.6e-32 0.17 1.00 YY1; CHAIN: C, ADENO-C 221 322 1.6e-32 0.17 1.00 YY1; CHAIN: C, ADENO-C 221 322 1.6e-32 0.17 1.00 YY1; CHAIN: C, ADENO-C 221 322 1.6e-32 0.17 1.00 YY1; CHAIN: C, ADENO-C 221 322 1.6e-32 0.17 1.00 YY1; CHAIN: C, ADENO-C 221 322 1.6e-32 0.17 1.00 YY1; CHAIN: C, ADENO-C 221 322 1.6e-32 0.17 1.00 YY1; CHAIN: C, ADENO-C 221 322 1.6e-32 0.17 1.00 YY1; CHAIN: C, ADENO-C 221 322 1.6e-32 0.17 1.00 YY1; CHAIN: C, ADENO-C 221 322 1.6e-32 0.17 1.00 YY1; CHAIN: C, ADENO-C 221 322 1.6e-32 0.17 1.00 YY1; CHAIN: C, ADENO-C 221 322 1.6e-32 0.17 1.00 YY1; CHAIN: C, ADENO-C 221 322 1.6e-32 0.17 1.00 YY1; CHAIN: C, ADENO-C 221 322 1.6e-32 0.17 1.00 YY1; CHAIN: C, ADENO-C 221 322 1.6e-32 0.17 1.00 YY1; CHAIN: C, ADENO-C 221 322 1.6e-32 0.17 1.00 YY1; CHAIN: C, ADENO-C 221 322 0.17 1.00 YY1; CHAIN: C, ADENO-C 221 0.17 1.00 YY1; CHAIN: C, ADENO-C 221 0.17 1.00 YY1; CHAIN: C, ADE	=			186		7.5e-48	0.35	1.00		YY1; CHAIN: C; ADENO.	COMPLEX (TRANSCRIPTION
C 217 322 7.5e-51 0.15 1.00 YYI; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INTITATOR ELEMENT DNA; CHAIN: A, B; CHAIN: A, B; CHAIN: A, B; CHAIN: C, ADENO-C 221 322 1.6e-32 0.17 1.00 YYI; CHAIN: C; ADENO-C 221 322 1.6e-32 0.17 1.00 YYI; CHAIN: C; ADENO-C 221 322 1.6e-32 0.17 1.00 YYI; CHAIN: C; ADENO-C 221 322 1.6e-32 0.17 1.00 YYI; CHAIN: C; ADENO-C 221 322 1.6e-32 0.17 1.00 YYI; CHAIN: C; ADENO-C							-			ASSOCIATED VIRUS PS	REGULATION/DNA) YING-YANG 1;
C 217 322 7.5e-51 0.15 1.00 YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B; CHAIN: A, B; CHAIN: C, ADENO-C 221 322 1.6e-32 0.17 1.00 YY1; CHAIN: C; ADENO-C CHAIN: C, ADENO-C C C C C C C C C C C C C C C C C C C					•	. 40				INITIATOR ELEMENT DNA;	I KANSCKIPTION INITIATION,
C 217 322 7.5e-51 0.15 1.00 YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B; CHAIN: A, B; CHAIN: C, ADENO-C 221 322 1.6e-32 0.17 1.00 YY1; CHAIN: C, ADENO-C CHAIN: C, ADENO-C CHAIN: C, ADENO-C CHAIN: C, ADENO-C C CAIN C, ADENO-C C CAIN C, ADENO-C C C C C C C C C C C C C C C C C C C									·	Citative Page	FINGER PROTEIN DNA-PROTEIN
C 217 322 7.5e-51 0.15 1.00 YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B; CHAIN: A, B; CHAIN: C, ADENO-C 221 322 1.6e-32 0.17 1.00 YY1; CHAIN: C; ADENO-											RECOGNITION, 3 COMPLEX
C 217 322 7.5e-51 0.15 1.00 YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B; CHAIN: A, B; CHAIN: C, ADENO-C 221 322 1.6e-32 0.17 1.00 YY1; CHAIN: C, ADENO-											(TRANSCRIPTION
C 221 322 1.6e-32 0.17 1.00 YY1; CHAIN: C; ADENO-	ΙΞ	+	-	217	\dagger	7 50.51	210	8		VAVI. OTTABLO, ABRIDO	REGULATION/DNA)
CHAIN: A, B; C 221 322 1.6e-32 0.17 1.00 YY1; CHAIN: C; ADENO-	3		-			10.50.	-	3	-	ASSOCIATED VIBIS PS	COMPLEX (IRANSCRIPTION REGIT ATTOM/DNA) VANG VANG 1:
CHAIN: A, B; C 221 322 1.6e-32 0.17 1.00 YY1; CHAIN: C; ADENO-									-	INITIATOR ELEMENT DNA:	TRANSCRIPTION INITIATION
C 221 322 1.6e-32 0.17 1.00 YY1; CHAIN: C; ADENO-										CHAIN: A, B;	INITIATOR ELEMENT, YY1, ZINC 2
RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DELASCRIPTION REGULATION/DELASCRIPTION C 221 322 1.66-32 0.17 1.00 YY1; CHAIN: C; ADENO- COMPLEX (TRANSCRIPTION-			, , , .			•			•		FINGER PROTEIN, DNA-PROTEIN
C 221 322 1.66-32 0.17 1.00 YY1; CHAIN: C; ADENO- COMPLEX (TRANSCRIPTION						•			,,		RECOGNITION, 3 COMPLEX
C 221 322 1.6e-32 0.17 1.00 YY1; CHAIN: C; ADENO-		•									ł
	23			221	322		0.17	1.00		YY1; CHAIN: C; ADENO-	COMPLEX (TRANSCRIPTION

			104000000000000000000000000000000000000		,,,,,, <u></u>
PDB annotation	REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION)	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION)	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INTTATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, DOCUMENTEX (TRANSCRIPTION REGULATION/DNA)	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION)	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION,
Coumpound	ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	YYI; CHAIN: C; ADENO- ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	YY1; CHAIN: C; ADENO- ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	YYI; CHAIN: C; ADENO- ASSOCIATED VIRUS PS INITIATOR ELEMENT DNA; CHAIN: A, B;	YYI; CHAIN: C; ADENO. ASSOCIATED VIRUS PS INITIATOR ELEMENT DNA;
SEQFOL D score					
PMF		66.0	-0.02	0.64	0.36
Verify score		-0.16	0.04	0.23	0.26
Psi Blast		3.2e-26	1.6e-24	1.5e-30	6.4e-29
END		377	453	509	481
STAR T AA		249	305	351	360
CHAI N ID	:	ပ	o	ပ	၁
PDB ID		lubd	Iubd	lubd	Jubd
SEQ NO:		1801	1801	1801	1801

PDB annotation	INITIATOR ELEMENT, YYI, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)	COMPLEX (TRANSCRIPTION REGULATION/DERPENG-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)	COMPLEX (TRANSCRIPTION REGULATIONDNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION)	
Coumpound	CHAIN: A, B;	YYI; CHAIN: C; ADENO- ASSOCIATED VIRUS P5 INTIATOR ELEMENT DNA; CHAIN: A, B;	YYI; CHAIN: C; ADENO- ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	YYI; CHAIN: C; ADENO. ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX(TRANSCRIPTION REGULATIONDNA) TRAMTRACK PROTEIN (TWO ZINC-FINGER PEPTIDE) COMPLEXED WITH 2DRP 3
SEQFOL D score					
PMF		0.65	1.00	86.0	0.10
Verify		0.07	0.30	-0.10	0.53
Psi Blast		3.26-31	4.56-40	86-34	3e-18
END AA		509	565	595	377
STAR T AA		387	454	464	294
CHAI N ID		o •	O	ວ	¥
PDB ID		1npq	lubd	lubd	2drp
SEQ D NO:		080 11	1801	1801	1801

PDB annotation		COMPLEX (DNA-BINDING	GLI, ZINC FINGER, COMPLEX (DNA-	BINDING PROTEIN/DNA)	COMPLEX (DNA-BINDING	FRUIEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-	BINDING PROTEIN/DNA)	COMPLEX (DNA-BINDING	PROTEIN/DNA) FIVE-FINGER GLI;	GLI, ZINC FINGER, COMPLEX (DNA-	BINDING PROTEIN/DNA)	COMPLEX (DNA-BINDING	PROTEIN/DNA) FIVE-FINGER GLI;	GLI, ZINC FINGER, COMPLEX (DNA-	BINDING PROTEIN/DNA)	COMPLEX (DNA-BINDING	PROTEIN/DNA) FIVE-FINGER GLI;	GLI, ZINC FINGER, COMPLEX (DNA-	BINDING PROTEIN/DNA)	COMPLEX (DNA-BINDING	PROTEIN/DNA) FIVE-FINGER GLI;	GLI, ZINC FINGER, COMPLEX (DNA-	BINDING PROTEIN/DNA)	COMPLEX (DNA-BINDING	PROTEIN/DNA) FIVE-FINGER GLI;	GLI, ZINC FINGER, COMPLEX (DNA-	BINDING PROTEIN/DNA)	COMPLEX (DNA-BINDING	PROTEIN/DNA) FIVE-FINGER GLI;	GLI, ZINC FINGER, COMPLEX (DNA-	BINDING PROJEIN/DNA)	COMPLEX (DNA-BINDING
Coumpound	DNA 2DRP 4	ZINC FINGER PROTEIN GLII;	Chain: A; DivA; Chain: C, D;		ZINC FINGER PROTEIN GLII;	CHAIN: A; DNA; CHAIN: C, U;		ZINC FINGER PROTEIN GLI1;	CHAIN: A; DNA; CHAIN: C, D;			ZINC FINGER PROTEIN GLII;	CHAIN: A; DNA; CHAIN: C, D;			ZINC FINGER PROTEIN GLI1;	CHAIN: A; DNA; CHAIN: C, D;	,		ZINC FINGER PROTEIN GLII;	CHAIN: A; DNA; CHAIN: C, D;			ZINC FINGER PROTEIN GLII;	CHAIN: A; DNA; CHAIN: C, D;			ZINC FINGER PROTEIN GLII;	CHAIN: A; DNA; CHAIN: C, D;		ייייי זיי זיי זייייי מיייי מיייי מיייי מיייי	ZINC FINGER PROJEIN GEII;
SEQFOL D score		100.58																mar of the same				-			100							
PMF score					8.			06'0				0.81				0.49				-0.02		•		0.87				0.75			9	70.0
Verify score			•		0.25			0.15				0.01				0.11				0.15				0.40				0.25			000	0.37
Psi Blast		1.ie-58			3e-57			1.1e-58				3.2e-23				1.1e-37				8e-30				6.4e-32				1.5e-48		798 (10 d m	,	1.00-33
END		296			236			322				\$				511				208				536	-		ļ	565			1772	5
STAR T AA		157			157			185				249				297				360				424				428			436	2
CHAI N ID		Ą		,	∢			¥				∢				∢				~_				∢				₽.			Ψ	¢
PDB ID		2gli		:	2gli			2gli				2gli				2gli				2gli				2gli				. 2gn			20li	£611
SEQ ID NO:		1801			1801			1801				1801				1801				1801				1801				1801			1801	1001

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PDB annotation	PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA- BINDING PROTEIN/DNA)	LECTIN CL-QPDWG; 1AFB 7 C-TYPE LECTIN, CALCIUM-BINDING PROTEIN 1AFR 22	SUGAR BINDING PROTEIN C-TYPE SUGAR BINDING PROTECTIN, LECTIN, CRD, SP-D, COLECTIN, ALPHA-HELICAL COLLED- 2 COIL, LAUGS SURFACTANT, SUGAR BINDING PROTEIN	NK CELL NK CELL, RECEPTOR, C. TYPE LECTIN, C-TYPE LECTIN- LIKE, NKD	NK CELL NK CELL, RECEPTOR, C. TYPE LECTIN, C-TYPE LECTIN- LIKE, NKD	COLLAGEN BINDING PROTEIN IX- BP; IX-BP; COAGULATION FACTOR IX-BINDING, HETERODIMER, VENOM, HABU 2 SNAKE, C-TYPE LECTIN SUPERFAMILY, COLLAGEN BINDING PROTEIN	MEMBRANE PROTEIN SP-A; SP-A:PHOSPHOLIPID MOLOLAYER COMPLEX	SIGNALING PROTEIN HEPATIC LECTIN HI: C-TYPE LECTIN CRD	SIGNALING PROTEIN HEPATIC LECTIN HI: C-TYPE LECTIN CRD	HEMATOPOIETIC CELL RECEPTOR ACTIVATION INDUCER MOLECULE (AIM), EA 1, HEMATOPOIETIC CELL
Coumpound	CHAIN: A; DNA; CHAIN: C, D;	MANNOSE-BINDING PROTEIN- A; LAFB 4 CHAIN: 1, 2, 3; LAFB	LUNG SURFACTANT PROTEIN D; CHAIN: A, B, C;	CD94; CHAIN: NULL;	CD94; CHAIN: NÜLL;	COAGULATION FACTOR IX- BINDING PROTEIN A; CHAIN: A; COAGULATION FACTOR IX- BINDING PROTEIN B; CHAIN: B;	SURFACTANT PROTEIN A; CHAIN: A;	ASIALOGLYCOPROTEIN RECEPTOR 1: CHAIN: A:	ASIALOGLYCOPROTEIN RECEPTOR 1; CHAIN: A;	EARLY ACTIVATION ANTIGEN CD69; CHAIN: A;
SEQFOL D score		59.81		74.73		67.59				
PMF			0.83		0.98		0.18	1.00	0.48	0.65
Verify score			0.35		0.57		0.06	0.47	0.35	0.79
Psi Blast		1.5e-21	3e-31	4.5e-29	4.5e-29	8e-25	1.2e-27	1,5e-28	1.6e-28	1.5e-27
END		252	249	253	251	250	249	250	252	250
STAR T AA		68	118	123	126	125	103	126	126	125
CHAI N ID		·	¥			∀	A	A	Ą	Ą
PDB ID		1afb	1508	1b6e	156e	16j3	1du8	Idv8	1dv8	1e87
SEQ ID NO:		1802	1802	1802	1802	1802	1802	1802	1802	1802

PDB annotation	RECEPTOR, LEUCOCYTE, C-TYPE		-	IXX-BP COAGULATION FACTOR	BINDING, C. TYRYLECTIN, GLA.	DOMAIN 2 BINDING, C-TYPE CRD MOTIF 1.00P EXCHANGED DIMFR	COAGULATION FACTOR BINDING	LX/X-BP COAGULATION FACTOR	BINDING, C-TYPE LECTIN, GLA-	DOMAIN 2 BINDING, C-TYPE CRD	MOTIF, LOOP EXCHANGED DIMER	PANCREATIC STONE INHIBITOR	PANCREATIC STONE INHIBITOR,		•••	FANCKEALIC STONE PROTEIN, PSP;	PANCREATIC STONE INHIBITOR,	1		PANCREATIC STONE PROTEIN, PSP.	PANCREATIC STONE INHIBITOR,			_					1 YPE LECTIN-LIKE, 2	HISTOCOMPATIBILITY, B2M, LY49,
Coumpound		MANNOSE-BINDING PROTEIN; 1HIP 4 CHAIN: NITI.: 1HIP 5	COAGULATION FACTORS	IX/X-BINDING PROTEIN;	CHAIN: A, B, C, D, E, F;		COAGULATION FACTORS	IX/X-BINDING PROTEIN;	CHAIN: A, B, C, D, E, F;			LITHOSTATHINE; CHAIN:	NOLL		LITHOSTATHINE; CHAIN: A;				LITHUSTATHINE; CHAIN: A;				MHC CLASS I H-2DD HEAVY	CHAIN; CHAIN: A; BETA-2-	MICROGLOBULIN; CHAIN: B;	HIV ENVELOPE	GLYCOPROTEIN 120 PEPTIDE;	CHAIN: P; LY49A; CHAIN: C, D;		
SEQFOL D score		63.07	65.37		_		61.47				35,0	% % %							5.1.				-							
PMF score														000	0.80								0.60							
Verify															C.:								0.60							
Psi Blast		3e-27	1e-24				6e-25				30.06	25-23		35.00	26-28			90.30	07-20				1.5e-30							
END		249	250				252				250	767		25.0	707			250	707				553							
STAR		86	125				125				106	25.		114	+			114	<u>+</u>			.55	571							
CHAI N ID			¥			•	В								ς .				ς .			,	ر							
PDB ID		Jhup	1ixx				lixx		and company		:	1		1000	na h	_		1001	no.hr	٠.		1	cabi							
SEQ NO:		1802	1802				1802				1800	7001		1973	1902			1800	1			2001	7001							

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PDB annotation	COMPLEX (NK RECEPTOR/MHC CLASS I) H-2 CLASS I HISTOCOMPATIBILITY ANTIGEN, B2M; NK-CELL SURFACE GLYCOPROTEIN YEI/48, NK CELL, NHIBITORY RECEPTOR, MHC-I, C- TYPE LECTIN-LIKE, 2 HISTOCOMPATIBILITY, B2M, LY49, 1.Y-49	LECTIN SUB-MBP-C; IRDL 9 C-TYPE LECTIN, CALCIUM-BINDING PROTEIN IRDL 20		ANTIFREEZE PROTEIN RECOMBINANT SEA RAVEN PROTEIN, SOLUTION BACKBONE FOLD, C- 2 TYPE LECTIN, ANTIFREEZE PROTEIN		LECTIN CL-QPDWG; 1AFB 7 C-TYPE LECTIN, CALCIUM-BINDING PROTEIN 1AFB 22	SUGAR BINDING PROTEIN C-TYPE LECTIN, CRD, SP-D, COLECTIN, ALPHA-HELICAL COILED- 2 COIL, LUNG SURFACTANT, SUGAR
Coumpound	MHC CLASS I H-2DD HEAVY CHAIN; CHAIN: A; BETA-2- MICROGLOBULIN; CHAIN: B; HIV ENVELOPE GLYCOPROTEIN 120 PEPTIDE; CHAIN: P; LY49A; CHAIN: C, D;	MANNOSE-BINDING PROTEIN- C; IRDL 6 CHAIN: 1, 2; IRDL 7	LECTIN MANNOSE-BINDING PROTEIN A (CLOSTRIPAIN FRAGMENT) (CL-MBP-A) IRTM 3 IRTM 96	SEA RAVEN TYPE II ANTIFREEZE PROTEIN; CHAIN: A;	LECTIN MANNOSE-BINDING PROTEIN A (LECTIN DOMAIN) COMPLEX WITH 2MSB 3 CALCIUM AND GLYCOPEPTIDE 2MSB 4	MANNOSE-BINDING PROTEIN- A; 1AFB 4 CHAIN: 1, 2, 3; 1AFB	LUNG SURFACTANT PROTEIN D; CHAIN: A, B, C;
SEQFOL D score		61.44	63.45		61.86	60.17	
PMF score	0.43			0.41			0.83
Verify score	0.81	·		0.52			0.35
Psi Blast	1.3e-27	1.2e-26	4.5e-23	1.3e-29	1.3e-25	1.5e-21	
END AA	233	251	252	250	251	291	288
STAR T AA	130	136	68	123	136	127	157
CATAI N ID	Q	1	1	4	· ·		Ą
PDB CI	1403	lrdi	Irtm	2afp	2msb	lafb	1508
SEQ ID	1802	1802	1802	1802	1802	1803	1803

PDB annotation	BINDING PROTEIN	NK CELL NK CELL, RECEPTOR, C. TYPE LECTIN, C-TYPE LECTIN- LIKE, NKD	NK CELL NK CELL, RECEPTOR, C. TYPE LECTIN, C-TYPE LECTIN- 1 KF NKD	COLLAGEN BINDING PROTEIN IX- BP; IX-BP; COAGULATION FACTOR IX-BINDING HETEPODINGED	VENOM, HABU 2 SNAKE, C-TYPE LECTIN SUPERFAMILY, COLLAGEN RINDING PROTEIN	COLLAGEN BINDING PROTEIN IX-	BP; IX-BP; COAGULATION FACTOR IX-BINDING, HETERODIMER,	VENOM, HABU 2 SNAKE, C-TYPE	BINDING PROTEIN	MEMBRANE PROTEIN C-TYPE LECTIN-LIKE DOMAINS		MEMBRANE PROTEIN SP-A; SP-	A:PHOSPHOLIPID MOLOLAYER COMPLEX	SIGNALING PROTEIN HEPATIC	LECTIN HI; C-TYPE LECTIN CRD	SIGNALING PROTEIN HEPATIC	LECTIN HI; C-TIPPE CETIN CRD	HEMATOPOIETIC CELL RECEPTOR ACTIVATION INDICER MOLECITE	(AIM). EA 1. HEMATOPOIETIC CELL	RECEPTOR, LEUCOCYTE, C.TYPE
Coumpound		CD94; CHAIN: NULL;	CD94; CHAIN: NULL;	COAGULATION FACTOR IX- BINDING PROTEIN A; CHAIN: A: COAGH ATION FACTOR IX-	BINDING PROTEIN B; CHAIN: B;	COAGULATION FACTOR IX-	BINDING PROTEIN A; CHAIN: A; COAGULATION FACTOR IX-	BINDING PROTEIN B; CHAIN:	ia î	FLAVOCETIN-A: ALPHA SUBUNIT; CHAIN: A;	FLAVOCETIN-A: BETA SUBUNIT; CHAIN: B	SURFACTANT PROTEIN A;	CHAIN: A;	ASIALOGLYCOPROTEIN	RECEPTOR 1; CHAIN: A;	ASIALOGLYCOPROTEIN	RECEPTOR 1; CHAIN: A;	EARLY ACTIVATION ANTIGEN CD69: CHAIN: A:		
SEQFOL D score		73.97		68.01															-	
PMF score			86.0			0.48				90'0-		0.18	•	0.46		00.1		0.65	_	
Verify score			0.57			0.16				0.38		0.06		0.13		0.47		0.79		,
Psi Blast		4.5e-29	4.5e-29	1e-24		1e-24				4.5e-24		1.2e-27		4.8e-25		1.5e-28		1.5e-27		
END		292	290	289		288				290		288		288		582		289		
STAR T AA		162	165	164		165				165		142		165		165		164		
CHAI N ID				Ą		Ą				м		4		Ą		∢		∢		
PDB ID		1b6e	166e	1bj3		1bj3				1c3a		1du8		1dv8		TOVS		le87		
SEQ ID NO:		1803	1803	1803		1803			·	1803		1803		1803	5007	5081		1803		

PDB annotation	LECTIN-LIKE, 2 NKD, KLR	SUGAR BINDING PROTEIN C-TYPE LECTIN, MANNOSE RECEPTOR	C-TYPE LECTIN ALPHA-HELICAL	C-TYPE LECTIN ALPHA-HELICAL	COLLED-COIL 1HUP 12	COAGULATION FACTOR BINDING	LX/X-BF COAGULATION FACTOR BINDING, C-TYPE LECTIN, GLA-	DOMAIN 2 BINDING, C-TYPE CRD	MOTIF, LOOP EXCHANGED DIMER	COAGULATION FACTOR BINDING	IX/X-BF COAGULATION FACTOR	DOMAIN SENDING CAVE CRD	MOTIF, LOOP EXCHANGED DIMER	COAGULATION FACTOR BINDING	IXX-BP COAGULATION FACTOR	BINDING, C-TYPE LECTIN, GLA-	DOMAIN 2 BINDING, C-TYPE CRD	MOTIF, LOOP EXCHANGED DIMER	COAGULATION FACTOR BINDING	IX/X-BP COAGULATION FACTOR	NDING, C-TYPE LECTIN, GLA-	DOMAIN 2 BINDING, C-TYPE CRD	MOTIF, LOOP EXCHANGED DIMER	PANCREATIC STONE INHIBITOR	PANCREATIC STONE INHIBITOR,	PANCEFATIC STONE INHIBITION	PANCREATIC STONE INHIBITOR,	METAL BINDING PROTEIN
Coumpound		MACROPHAGE MANNOSE SU RECEPTOR; CHAIN: A, B;	TEIN;	-	JP 5	S	CHAIN: A. B. C. D. E. F:			···	·	Circle (A, D, C, D, E, F;	Σ	S	ż	CHAIN: A, B, C, D, E, F;) <u>U</u>		<u> </u>	'	CHAIN: A, B, C, D, E, F; BI	<u>)</u>		OSTATHINE; CHAIN:	NULL	1 ITHOSTATHINE: CHAIN: PA		LITHOSTATHINE; CHAIN: A; MI
SEQFOL D score			63.43			65.74				-				61.53										•		67.30		
PMF score		\$6.0		0.40						0.48									0.48					0.89				0.86
Verify score		0.62		0.33						0.32	-								0.38					0.77	-21			0.75
Psi Blast		1.5e-25	3e-27	3e-27		1e-24			,	1e-24				6e-25					6e-25					3e-25		30-25	:	3e-28
END		288	288	289		289			3	288				291					290					291		291	<u> </u>	291
STAR T AA		165	150	164		164				165				164					165					165		165	}	153
CEAI N ID		¥	į			₹				∢				В					щ			•					_	Ą
PDB ID		legg	1hup	Ihup		ii X			,	X			_	ii. X					lix			- 123		III		111		lqdd
SEQ ID NO:		1803	1803	1803		1803			000	1803				1803					1803					1803		1803		1803

PDB annotation	PANCREATIC STONE PROTEIN, PSP. PANCREATIC STONE INHIBITOR, LITHOSTATHINE	METAL BINDING PROTEIN PANCREATIC STONE PROTEIN, PSP; PANCREATIC STONE INHIBITOR, LITHOSTATHINE	COMPLEX (NK RECEPTOR/MHC CLASS I) H-2 CLASS I HISTOCOMPATIBILITY ANTIGEN, B2M; NK-CELL SARGACE	GLYCOPROTEIN YEI/48, NK CELL, INHIBITORY RECEPTOR, MHC-1, C- TYPE LECTIN-LIKE, 2 HISTOCOMPATIBILITY, B2M, LY49, LY-49	COMPLEX (NK RECEPTORMHC CLASS I) H-2 CLASS I HISTOCOMPATIBILITY ANTIGEN, B2M; NK-CELL SURFACE GLYCOPROTEIN YEI/48, NK CELL, INHIBITORY RECEPTOR, MHC-I, C- TYPE LECTIN-LIKE, 2 HISTOCOMPATIBILITY, B2M, LY49, LY-49	LECTIN SUB-MBP-C; IRDL 9 C-TYPE LECTIN, CALCIUM-BINDING PROTEIN IRDL 20	LECTIN SUB-MBP-C; IRDL 9 C-TYPE LECTIN, CALCIUM-BINDING PROTEIN IRDL 20	
Coumpound		LITHOSTATHINE; CHAIN: A;	MHC CLASS I H-2DD HEAVY CHAIN; CHAIN: A; BETA-2- MICROGLOBULIN; CHAIN: B; HIV ENVELOPE	GLYCOPROTEIN 120 PEPTIDE; CHAIN: P; LY49A; CHAIN: C, D;	MHC CLASS I H-2DD HEAVY CHAIN; CHAIN: A; BETA-2- MICROGLOBULN; CHAIN: B; HIV ENVELOPE GLYCOPROTEIN 120 PEPTIDE; CHAIN: P; LY49A; CHAIN: C, D;	MANNOSE-BINDING PROTEIN. C; 1RDL 6 CHAIN: 1, 2; 1RDL 7	MANNOSE-BINDING PROTEIN. C; IRDL 6 CHAIN: 1, 2; IRDL 7	LECTIN MANNOSE-BINDING PROTEIN A (CLOSTRIPAIN FRAGMENT) (CL-MBP-A) IRTM
SEQFOL D score		73.96				61.70	<u> </u>	64.49
PMF			0.60		0,43		0.70	
Verify score			0.60		0.81		0.41	
Psi Blast		3e-28	1.5e-30		1.36-27	1.2e-26	1.2e-26	4.5e-23
END		291	292	·	292	290	289	291
STAR T AA		153	791		169	175	176	127
CEAI N ID		A	ပ	•	Д	,·	g-mag	1
PDB ID		Iqdd	1903		1903	1rdi	Indi	1rtm
SEQ ID NO:		1803	1803		1803	1803	1803	1803

PDB annotation		ANTIFREEZE PROTEIN RECOMBINANT SEA RAVEN PROTEIN, SOLUTION BACKBONE FOLD, C- 2 TYPE LECTIN, ANTIFREEZE PROTEIN			HYDROLASE CALCINEURIN; HYDROLASE, PHOSPHATASE, IMMUNOSUPPRESSION			CALCIUM-BINDING PROTEIN CALMODULIN APO TR2C-DOMAIN;	METAL TRANSPORT CALMODULIN, HIGH RESOLUTION, DISORDER
Coumpound	3 IRTM 96	SEA RAVEN TYPE II ANTIFREEZE PROTEIN; CHAIN: A;	LECTIN MANNOSE-BINDING PROTEIN A (LECTIN DOMAIN) COMPLEX WITH 2MSB 3 CALCIUM AND GLYCOPEPTIDE 2MSB 4	LECTIN MANNOSE-BINDING PROTEIN A (LECTIN DOMAIN) COMPLEX WITH 2MSB 3 CALCIUM AND GLYCOPEPTIDE 2MSB 4	SERINE/THREONINE PHOSPHATASE 2B; CHAIN: A, B;	CALCTUM-BINDING PROTEIN CALMODULIN COMPLEXED WITH CALMODULIN-BINDING DOMAIN OF 1CDM 3 CALMODULIN-DEPENDENT PROTEIN KINASE II 1CDM 4	CALCIUM-BINDING PROTEIN CALMODULIN (VERTEBRATE) ICLL 3	CALMODULIN (VERTEBRATE); ICMF 6 CHAIN: NULL; ICMF 7	CALMODULIN; CHAIN: A;
SEQFOL D score			98.19						
PMF		0.41		0.54	0.87	0.36	0.49	0.60	0.93
Verify score		0.52		0.57	0.10	-0.07	-0.04	0.23	0.11
Psi Blast		1.3e-29	1,3e-25	1.3e-25	4.86-24	1.6e-29	8e-36	8e-32	9.6e-34
END		289	290	288	80	18	180	81	81
STAR T AA		162	175	176			-	∞	-
CHAI N ID		¥	∢	¥	æ	¥			4
PDB TD		2afp	2msb	2msb	lani	m .	Icli	lcmf	lexr
SEQ ID NO:		1803	1803	1803	1804	1804	1804	1804	1804

<u></u>				,		-,·			
PDR sunotation		TRANSPORT PROTEIN CALCIUM BINDING, EF HAND, FOUR-HELIX BUNDLE	CALCIUM-REGULATED MUSCLE CONTRACTION MUSCLE CONTRACTION, CALCIUM- BINDING, TROPONIN, E-F HAND, 2 OPEN CONFORMATION REGULATORY DOMAIN, CALCIUM- REGULATED 3 MUSCLE CONTRACTION			CALMODULIN, CALCIUM BINDING, HELIX-LOOP-HELIX, SIGNALLING, 2 COMPLEX(CALCIUM-BINDING PROTEIN/PEPTIDE)	COMPLEX (NUCLEAR PROTEINRNA) COMPLEX (NUCLEAR PROTEINRNA), RNA, SNRND PROMITCI ROPPOTEN	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA, ENDAR PROTEIN/RNA), RNA,	CELL ADHESION LEUCINE RICH REPEAT, CALCIUM BINDING, CELL
Commoning		CALMODULIN; CHAIN: A;	TROPONIN C; CHAIN: NULL;	CONTRACTILE SYSTEM PROTEIN TROPONIN C 110P 3	CALCIUM BINDING PROTEIN CALMODULIN (TR=2=C\$ FRAGMENT COMPRISING RESIDUES 78 - 148 1TRC 3 OF THE INTACT MOLECULE) 1TRC 4	CALMODULIN; CHAIN: A; RS20; CHAIN: B;	U2 RNA HAIRPIN IV; CHAIN: Q, R; U2 A'; CHAIN: A, C; U2 B"; CHAIN: B, D;	U2 RNA HAIRPIN IV; CHAIN: Q. R; U2 A; CHAIN: A, C; U2 B"; CHAIN: B, D;	INTERNALIN B; CHAIN: A;
SEOFOI.	D score								
PIMIR	score	0.89	1.00	0.95	0.98	0.98	1.00	0.99	0.98
Verify	score	0.39	0.23	0.25	0.52	0.30	0.60	0.58	0.57
Psi Blast		8e-30	1.6e-24	1.6e-24	1.4e-30	3.2e-35	8e-24	8e-24	6.4e-34
END	AA	81	<u></u>	81	₩	83	250	250	727
STAR	TAA	14	-	_	21		114	114	44
CHAI	E E	Ą			¥	₹	4	၁	4
PDB	<u>a</u>	1771	1tef	Itop	ltrc	l vrk	1а9п	la9n	1d0b
SEO	NO.	1804	1804	1804	1804	1804	1806	1806	1806

PDB annotation	ADHESION	CELL ADHESION LEUCINE RICH REPEAT, CALCIUM BINDING, CELL ADHESION	TRANSFERASE CRYSTAL	STRUCTURE, RAB	GERANYLGERANYLTRANSFERASE,	2.0 A 2 RESOLUTION, N-	FORMYLMETHIONINE, ALPHA	SUBUNIT, BETA SUBUNIT	The A Moreon A on Character A I	STRUCTURE, RAB	GERANYLGERANYLTRANSFERASE.	2.0 A 2 RESOLUTION, N-	FORMYLMETHIONINE, ALPHA	SUBUNIT, BETA SUBUNIT		CONTRACTILE PROTEIN LEUCINE-	RICH REPEAT, BETA-BETA-ALPHA	CYLINDER, DYNEIN, 2	CHLAMYDOMONAS, FLAGELLA	CONTRACTILE PROTEIN LEUCINE-	RICH REPEAT, BETA-BETA-ALPHA	CYLINDER, DYNEIN, 2	CHLAMYDOMONAS, FLAGELLA	CONTRACTILE PROTEIN LEUCINE-	RICH REPEAT, BETA-BETA-ALPHA	CYLINDER, DYNEIN, 2	CHLAMYDOMONAS, FLAGELLA	D	COMPLEX (HSP24/HSP70) HSP70,	GRPE, MOLECULAR CHAPERONE,	NOCEEU INDE EACEMINGE 4
Coumpound		INTERNALIN B; CHAIN: A;	RAB	GERANYLGERANYLTRANSFE	RASE ALPHA SUBUNIT;	CHAIN: A, C; RAB	GERANYLGERANYLTRANSFE	RASE BETA SUBUNIT; CHAIN:	1, 7, 0 A0	GERANYLGERANYLTRANSFE	RASE ALPHA SUBUNIT;	CHAIN: A, C; RAB	GERANYLGERANYLTRANSFE	RASE BETA SUBUNIT; CHAIN:	B, D;	OUTER ARM DYNEIN; CHAIN:	A;			OUTER ARM DYNEIN; CHAIN:	A;	-		OUTER ARM DYNEIN; CHAIN:	A;				NUCLEOTIDE EXCHANGE	FACTOR GRPE; CHAIN: A, B;	היוסיים והיוסיים סיום סיום
SEQFOL D score																				•		-									
PMF score		00′1	66'0						000	900						0.78				0.46				0.01					0.11		
Verify score		0.39	0.51						0.48	ì						-0.40				-0.60				-030					-0.10		
Psi Blast		1.3e-32	3.2e-25						2 30 17							3e-14				1.6e-28				3.2e-13					0.0015		
END		235	249						202	ì						191				251				179					398		
STAR TAA		22	132				-		84	;						111				125				73					250		
CHAI N ID		4	Ą						4	:						Y				₹				∢					∢		
PDB ID		1406	1dce						1,400	}				_		1ds9				1ds9				1489					1dkg		
SEQ El SO NO:		1806	1806						1806	3						1806				1806				1806					1809		

PDB annotation	FACTOR, COLLED-COLL, COMPLEX (HSP24/HSP70)	ENDOCYTOSIS/EXOCYTOSIS NSEC1; PROTEIN-PROTEIN COMPLEX, MULTI-SUBUNIT	CONTRACTLE PROTEIN TRIPLE- HELIX COILED COIL, CONTRACTLE PROTEIN			HYDROLASE TARTRATE- RESISTANT ACID PHOSPHATASE; METAL PHOSPHATASE, HYDROLASE	HYDROLASE TARTRATE- RESISTANT ACID PHOSPHATASE; METAL PHOSPHATASE, HYDROLASE	HYDROLASE UTEROFERRIN, TRAP, PAP, TARTRATE RESISTANT ACID PURPLE ACID PHOSPHATASE, TARTRATE RESISTANT ACID 2 PHOSPHATASE, METALLOENZYME, ITEROFERRIN HYDROI ASE	HYDROLASE (PHOSPHORIC MONOESTER) PURPLE ACID PHOSPHATASE, HYDROLASE (PHOSPHORIC MONOESTER)
Coumpound	DNAK; CHAIN: D;	SYNTAXIN BINDING PROTEIN 1; CHAIN: A; SYNTAXIN 1A; CHAIN: B;	HUMAN SKELETAL MUSCLE ALPHA-ACTININ 2; CHAIN: A;	LIGASE(SYNTHETASE) SERYL- TRNA SYNTHETASE (E.C.6.1.1.11) (SERINE-TRNA LIGASE) ISES 3 COMPLEXED WITH SERYL-HYDROXAMATE-	AMP 1SES 4	PURPLE ACID PHOSPHATASE; CHAIN: A;	PURPLE ACID PHOSPHATASE; CHAIN: A;	II PURPLE ACID PHOSPHATASE; CHAIN: A;	PURPLE ACID PHOSPHATASE; CHAIN: A, B, C, D;
SEQFOL D score						61.74		63.06	
PMF score		-0.07	0.07	0.28			0.34		0.52
Verify		90:06	-0.12	0.21		æ	-0.19		0.01
Psi Blast		3e-08	7.5e-13	1.6e-05		4.5e-10	4.5e-10	0.00014	1.5e-12
END AA		367	374	528		310	239	320	247
STAR T AA		143	102	439		32	39	28	01
CHAI N ID		В	A	∢	+	Ą	A	¥	K
PDB ID		ldnI	lguu	1ses		Ідћw	1qhw	lute	4kbp
SEQ ID NO:		1809	1809	1812		1814	1814	1814	1814

1 - 1							
PDB annotation	RNA-BINDING ROCCENTRNA TRA PRE-MRNA; SPLICING REGULATION, RNP DOMAIN, RNA COMPLEX	STRUCTURAL PROTEIN PROTEIN C23; RNP, RBD, RRM, RNA BINDING DOMAIN, NUCLEOLUS	METAL TRANSPORT MRP8, S100A8, CALGRANULIN A CALCIUM-BINDING PROTEIN, CRYSTAL STRUCTURE, MAD, MIGRATION 2 INHIBITORY FACTOR RELATED PROTEIN 8, S100 PROTEIN		NUCLEAR PROTEIN UI SNRNP A PROTEIN; RNA BINDING DOMAIN, NUCLEAR PROTEIN	NUCLEAR PROTEIN UI SNRNP A PROTEIN; RNA BINDING DOMAIN, NUCLEAR PROTEIN	RNA BINDING DOMAIN RNA BINDING DOMAIN, RBD, RNA RECOGNITION MOTIF, RRM, 2 SPLICING INHIBITOR, TRANSLATIONAL INHIBITOR, SEX 3 DETERMINATION, X CHROMOSOME
Coumpound	SXL-LETHAL PROTEIN; CHAIN; A, B; RNA (5'- R(P*GP*UP*UP*UP*UP* UP*UP*UP*UP-CHAIN; P. 0;	NUCLEOLIN RBD2; CHAIN: A;	MIGRATION INHIBITORY FACTOR-RELATED PROTEIN 8; CHAIN: A, B;	RNA-BINDING PROTEIN SEX- LETHAL PROTEIN (C- TERMINUS, OR SECOND RNA- BINDING DOMAIN 1SXL 3 (RBD-2), RESIDUES 199 - 294 PLUS N-TERMINAL MET) 1SXL 4 (NMR, 17 STRUCTURES) 1SXL 5	UI SMALL NUCLEAR RIBONUCLEOPROTEIN A; CHAIN: NULL;	UI SMALL NUCLEAR RIBONUCLEOPROTEIN A; CHAIN: NULL:	SEX-LETHAL; CHAIN: A, B, C;
SEQFOL D score							
PMF	0.46	0.12	0.21	0.13	0.55	0.31	0.18
Verify	-0.30	-0.15	0.07	-0.32	0.29	0.31	-0.10
Psi Blast	3.2e-05	60-99'6	0.0045	3.2e-05	0.003	0.0093	6.4e-05
END	272	250	149	272	267	256	257
STAR T AA	195	180	101	195	881	261	195
CHAI N ID	∢ •	A	¥				∀
PDB ID	1b7f	1fjc	1mr8	1sx]	2u la	2ula	3sxl
SEQ NO:	1815	1815	1815	1815	1815	1815	1815

PDB annotation	DOSAGE COMPENSATION	HYDROLASE HOMODIMER, ALPHA/BETA HYDROLASE FOLD, DISUBSTITITED UREA 2 INHIBITOR	HYDROLASE HOMODIMER, ALPHA/BETA HYDROLASE FOLD, DISUBSTITUTED UREA 2 INHIBITOR	HYDROLASE HAD-FAMILY ALPHA'BETA CORE DOMAIN, MG(II) BINDING SITE, 5-2 HELIX BUNDLE	DEHALOGENASE DEHALOGENASE, HYDROLASE	ELECTRON TRANSPORT ELECTRON TRANSPORT, IRON-SULFUR	ELECTRON TRANSPORT ELECTRON TRANSPORT, IRON-SULFUR	ELECTRON TRANSFER (IRON- SULFUR PROTEIN)	ELECTRON TRANSPORT TWO 4FE- 4S CLUSTERS	HYDROGENASE HYDROGENASE, CYTOCHROME C553, ELECTRON TRANSFER COMPLEX	HYDROGENASE HYDROGENASE, CYTOCHROME C553, ELECTRON TRANSFER COMPLEX
Coumpound		EPOXIDE HYDROLASE; CHAIN: A, B;	EPOXIDE HYDROLASE; CHAIN: A, B;	PHOSPHONOACETALDEHYDE HYDROLASE; CHAIN: A, B, C, D;	L-2-HALOACID DEHALOGENASE; CHAIN: NULL;	7-FE FERREDOXIN; CHAIN: NULL;	7-FE FERREDOXIN; CHAIN: NULL;	FERREDOXIN; ICLF 5 CHAIN: NULL ICLF 6	2[4FE-4S] FERREDOXIN; CHAIN; A	[FE]-HYDROGENASE (LARGE SUBUNIT); CHAIN: A; [FE]-HYDROGENASE (SMALL SUBUNIT); CHAIN: D: CYNOLIN OF SEE CHAIN: D: CYNOLIN	[FE]-HYDROGENASE (LARGE SUBUNIT); CHAIN: A; [FE]- HYDROGENASE (SMALL SUBUNIT); CHAIN: D; CYTOCHROME C553; CHAIN: E
SEQFOL D score			-								·
PMF score		-0.14	0.05	9.64	-0.19	-0.19	-0.17	-0.17	-0.12	1.00	1.00
Verify		-0.00	-0.84	0.20	0.12	0.05	0.17	0.43	0.53	0.37	0,23
Psi Blast		3.2e-09	0.006	90-96	3e-10	8e-14	1.1e-10	1.1e-10	1.6e-11	6.4e-68	3 c -92
END		305	69	143	316	219	254	199	200	519	504
STAR T AA		172	39	38	28	137	176	137	137	136	173
CHAI N ID		A	æ	A					Ą	∢	Ą
PDB ID		leki	leki	Ifez	lzm	1bc6	1bc6	1cff	1dur	1e08	1e08
SEQ ID NO:		6181	1819	6181	6181	1820	1820	1820	1820	1820	1820

	PDB	CHAI	STAR	END	Psi Blast	Verify	PMF	SEQFOL	Coumpound	PDB annotation
ΘÖ	<u>e</u>	A E	TAA			score	score	D score		
1820	1 feh	Ą	1	574	1.4e-85			232.77	PERIPLASMIC HYDROGENASE 1; CHAIN: A;	OXIDOREDUCTASE OXIDOREDUCTASE
1820	lfeh	А	69	572	1.4e-85	0.33	1.00		PERIPLASMIC HYDROGENASE 1: CHAIN: A:	OXIDOREDUCTASE
1820	Ihfe	J	117	524	4.5e-92			223.69	FE-ONLY HYDROGENASE (SMALLER SUBUNIT); CHAIN: S, T; FE-ONLY HYDROGENASE (LARGER SUBUNIT); CHAIN: L,	HYDROGENASE FE-ONLY HYDROGENASE, X-RAY CRYSTALLOGRAPHY, HYDROGENE 2 METABOLISM, PERIPLASM
1820	1hfe	ū	122	519	3.2e-68	0.40	1.00		FE-ONLY HYDROGENASE (SMALLER SUBUNIT); CHAIN: S, T; FE-ONLY HYDROGENASE (LARGER SUBUNIT); CHAIN: L,	HYDROGENASE FE-ONLY HYDROGENASE, X-RAY CRYSTALLOGRAPHY, HYDROGENE 2 METABOLISM, PERIPLASM
1820	गिष्टि	7	173	504	4.5e-92	0.61	1.00		FE-ONLY HYDROGENASE (SMALLER SUBUNIT); CHAIN: S, T; FE-ONLY HYDROGENASE (LARGER SUBUNIT); CHAIN: L, M;	HYDROGENASE FE-ONLY HYDROGENASE, X-RAY CRYSTALLOGRAPHY, HYDROGENE 2 METABOLISM, PERIPLASM
1821	Icun	₩.	104	3 4	60-99	-0.18	0.01		ALPHA SPECTRIN; CHAIN: A, B, C;	STRUCTURAL PROTEIN TWO REPEATS OF SPECTRIN, ALPHA HELICAL LINKER REGION, 2.2 TANDEM 3-HELIX COILED-COILS, STRUCTURAL PROTEIN
1821	Icun	V	51	207	1.5e-07	-0.09	0.36	14 T	ALPHA SPECTRIN; CHAIN: A, B, C;	STRUCTURAL PROTEIN TWO REPEATS OF SPECTRIN, ALPHA HELICAL LINKER REGION, 2.2 TANDEM 3-HELIX COLLED-COLLS, STRUCTURAL PROTEIN
1821	lquu	A	54	302	9e-12	-		52.84	HUMAN SKELETAL MUSCLE ALPHA-ACTININ 2; CHAIN: A;	CONTRACTILE PROTEIN TRIPLE. HELIX COILED COIL, CONTRACTILE PROTEIN
1821	lquu	А	95	340	9e-12	-0.34	0.43		HUMAN SKELETAL MUSCLE	CONTRACTILE PROTEIN TRIPLE-

END Psi Blast Verify PMF SEQFOL AA score score D score	STAR END Psi Blast Verify PMF SEQFOL TAA AA score store D score	Psi Blast Verify PMF SEQFOL score score D score	ast Verify PMF SEQFOL score acore	PMF SEQFOL score D score	SEQFOL D score			Coumpound	PDB annotation
Y.	V.	V.	Y.	¥	V.	Y	K	ALPHA-ACTININ 2; CHAIN: A;	HELIX COLLED COLL, CONTRACTILE PROTEIN
L 29 125 9e-f/8	125 9e-08	96-08	25 15				4	ACTIVATED BROTTEN C.	COMMITTE STATE
							; E	CHAIN: C, L; D-PHE-PRO-MAI;	COAGULATION/INHIBITOR)
# <u>5</u>	# <u>5</u>	# <u>5</u>	# <u>5</u>	5	-	<u> </u>	5	CHAIN: P;	AUTOPROTHROMBIN IIA; HYDROLASE, SERINE
									PROTEINASE), PLASMA CALCIUM
									BINDING, 2 GLYCOPROTEIN, COMPLEX (BLOOD
							[COAGULATION/INHIBITOR)
45 113 6e-11 1.12 -0.15 HI	113 6e-11 1.12 -0.15	6e-11 1.12 -0.15	1.12 -0.15	-0.15		H	王	HIRUSTASIN; CHAIN: NULL;	ANTI-COAGULANT ANTI-
					-				COACOLEANI, FEI TIDIO INHIBITORS, CONFORMATIONAL 2
									FLEXIBILITY, SERINE PROTEASE
A 36 165 1.4e-26 0.53 -0.03 B	165 1.4e-26 0.53 -0.03	1.4e-26 0.53 -0.03	0.53 -0.03	-0.03		M	I CCC	BOWMAN-BIRK TRYPSIN	HYDROLASE INHIBITOR ALL-BETA
						 	j-rami	INHIBITOR; CHAIN: A	STRUCTURE, HYDROLASE
	126 1 Sp. 10 0 07 0.15	15-10 007 015	0.07	0.15			-11	Cun (AN) may morning	ACTIONAL TOWNS THE PROPERTY OF THE PARTY OF
C1.0- /0.0 61-0C.1 021 +	21.0- /8.0 61-00:1	1.3c-1 V.0 V.0	61.0-	21:5				BOWMAN-BIRK IRYPSIN	HYDROLASE INHIBITOR ALL-BETA STRICTION OF A SE
						1	-	Milleriols, Chalis, A	SINCTIONS, HIDROLASE INHIBITOR
L 2 135 7.5e-13 0.56 -0.19 E	135 7.5e-13 0.56 -0.19	7.5e-13 0.56 -0.19	0.56 -0.19	-0.19		ш.	щ	BLOOD COAGULATION	BLOOD COAGULATION, SERINE
				14	<u> </u>	<u> </u>	, page	FACTOR VIIA; CHAIN: L, H;	PROTEASE, COMPLEX, CO-FACTOR,
						-3 \	<i>,</i> ,	SOLUBLE HISSUE FACTOR;	Z RECEPTOR ENZYME, INHIBITOR,
							-	CHAIN: 1, U; D-PHE-PHE-ARG-	GLA, EGF, 3 COMPLEX (SERINE
							<i>-</i>	CHLUROME I HYLKE I ONE	PROTEASE/COFACTOR/LIGAND)
A 2 77 7.5e-11 1.08 -0.18	77 7.5e-11 1.08 -0.18	7.5e-11 1.08 -0.18	1.08 -0.18	-0.18			71	DEATH RECEPTOR 5: CHAIN:	APOPTOSIS TRAIL DRS COMPLEY
•	•	•	•	4	•	4	⋖	A. B. C. G. H. I: TNF-RELATED	
				7		7	~	APOPTOSIS INDUCING	
								LIGAND; CHAIN: D, E, F, J, K, L;	
A 31 125 4.5e-12 0.59 -0.12	125 4.5e-12 0.59 -0.12	4.5e-12 0.59 -0.12	0.59 -0.12	-0.12	• • • • • • • • • • • • • • • • • • • •			DEATH RECEPTOR 5; CHAIN:	APOPTOSIS TRAIL, DRS, COMPLEX
				-				A, B, C, G, H, I; TNF-RELATED	

PDB annotation		APOPTOSIS TRAIL, DR5, COMPLEX	SERINE PROTEINASE COAGULATION FACTOR II; COAGULATION FACTOR II; FETOMODULIN, TM, CD141 ANTIGEN, EGR-CMK SERINE PROTEINASE, EGF-LIKE DOMAINS, ANTICOAGULANT COMPLEX, 2 ANTIFIBRINOLYTIC COMPLEX	PLANT PROTEIN TWO HOMOLOGOUS HEVEIN-LIKE DOMAINS	PLANT PROTEIN TWO HOMOLOGOUS HEVEIN-LIKE DOMAINS	PLANT PROTEIN TWO HOMOLOGOUS HEVEIN-LIKE DOMAINS	SUGAR BINDING PROTEIN UDA; LECTIN, HEVEIN DOMAIN, UDA, SUPERANTIGEN	SUGAR BINDING PROTEIN UDA; LECTIN, HEVEIN DOMAIN, UDA, SUPERANTIGEN	SUGAR BINDING PROTEIN UDA; LECTIN, HEVEIN DOMAIN, UDA, SUPERANTIGEN	SUGAR BINDING PROTEIN UDA; LECTIN, HEVEIN DOMAIN, UDA,
Coumpound	APOPTOSIS INDUCING LIGAND; CHAIN; D, E, F, J, K, L;	DEATH RECEPTOR 5; CHAIN: A, B, C, G, H, I; TNF-RELATED APOPTOSIS INDUCING LIGAND: CHAIN: D, E, F, J, K, L;	THROMBIN LIGHT CHAIN; CHAIN: A, B, C, D; THROMBIN HEAVY CHAIN; CHAIN: M, N, O, P; THROMBOMODULIN; CHAIN: I, J, K, L; THROMBIN INHIBITOR L-GLU-L-GLY-L- ARM; CHAIN: E, F, G, H;	AGGLUTININ ISOLECTIN VI; CHAIN: A	AGGLUTININ ISOLECTIN VI; CHAIN: A	AGGLUTININ ISOLECTIN VI; CHAIN: A	AGGLUTININ ISOLECTIN VI/AGGLUTININ ISOLECTIN V; CHAIN: A;	AGGLUTININ ISOLECTIN VI/AGGLUTININ ISOLECTIN V; CHAIN: A;	AGGLUTININ ISOLECTIN VI/AGGLUTININ ISOLECTIN V; CHAIN: A;	AGGLUTININ ISOLECTIN VI/AGGLUTININ ISOLECTIN V;
SEQFOL D score										
PMF		-0.15	-0.14	-0.18	-0.12	0.16	0.17	-0.11	0.10	-0.17
Verify		1.17	0.58	0.49	1.11	1.00	0.87	1.02	1.08	0.24
Psi Blast		6e-12	4.5e-11	1.4e-18	7.5e-19	1.4e-18	1.5e-19	1.2e-19	1.5e-19	7.5e-17
END		96	155	111	91	141	121	06	141	160
STAR T AA		σ,	74	12	4	52	61	4	52	75
CHAI N ID		¥	p4	¥	4	А	А	A	Ą	Ą
PDB UD		1du3	1dx5	1chd	lehd	lehd	leis	leis	leis	leis
SEQ NO ID		1822	1822	1822	1822	1822	1822	1822	1822	1822

				,									
PDB annotation	SUPERANTIGEN	SUGAR BINDING PROTEIN UDA; LECTIN, HEVEIN DOMAIN, UDA, SUPERANTIGEN, SACCHARIDE BINDING	SUGAR BINDING PROTEIN UDA; LECTIN, HEVEIN DOMAIN, UDA, SUPERANTIGEN, SACCHARIDE BINDING	SUGAR BINDING PROTEIN UDA; LECTIN, HEVEIN DOMAIN, UDA, SUPERANTIGEN, SACCHARIDE BINDING	SUGAR BINDING PROTEIN UDA; LECTIN, HEVEIN DOMAIN, UDA, SUPERANTIGEN, SACCHARIDE BINDING	SIGNALLING PROTEIN BINDING PROTEIN, CYTOKINE, SIGNALLING PROTEIN	SIGNALLING PROTEIN BINDING PROTEIN, CYTOKINE, SIGNALLING PROTEIN	SIGNALLING PROTEIN BINDING PROTEIN, CYTOKINE, SIGNALLING PROTEIN	HORMONE RECEPTOR HORMONE RECEPTOR, INSULIN RECEPTOR FAMILY	GLYCOPROTEIN GLYCOPROTEIN	GLYCOPROTEIN GLYCOPROTEIN	GLYCOPROTEIN GLYCOPROTEIN	SIGNALLING PROTEIN TYPE I RECEPTOR, STNFRI; INCF 8
Coumpound	CHAIN: A;	AGGLUTININ ISOLECTIN VAGGLUTININ ISOLECTIN V/ CHAIN: A;	AGGLUTININ ISOLECTIN VAGGLUTININ ISOLECTIN V/ CHAIN: A;	AGGLUTININ ISOLECTIN I/AGGLUTININ ISOLECTIN V/ CHAIN: A;	AGGLUTININ ISOLECTIN VAGGLUTININ ISOLECTIN V/ CHAIN: A;	TUMOR NECROSIS FACTOR RECEPTOR; CHAIN: A, B;	TUMOR NECROSIS FACTOR RECEPTOR; CHAIN: A, B;	TUMOR NECROSIS FACTOR RECEPTOR; CHAIN: A, B;	INSULIN-LIKE GROWTH FACTOR RECEPTOR 1; CHAIN: A:	LAMININ; CHAIN: NULL;	LAMININ; CHAIN: NULL;	LAMININ; CHAIN: NULL;	TUMOR NECROSIS FACTOR RECEPTOR; INCF 4 CHAIN: A,
SEQFOL D score						62.34						82.39	50.41
PMF score		-0.13	-0.18	0.11	-0.14		-0.14	-0.14	-0.19	-0.15	-0.06		
Verify score		0,40	1.10	1.04	0.61		0.78	0.63	0.40	0.65	1.13		
Psi Blast		3e-18	6e-16	3e-21	6e-18	7.5e-20	7.5e-20	6e-i3	1.5e-28	1.2e-19	7.5e-27	7.5e-27	1.5e-12
END		121	8	141	160	177	175	128	178	178	155	157	171
STAR		12	2	52	79	10	12	ro.	4	47	4	4	34
CHAI N ID		Ą	Ą	¥	Ą	∀	¥	¥	¥				Ą
PDB cr		len2	len2	lem2	len2	lext	lext	lext	ligr	1klo	1klo	Iklo	lncf
SEQ No:		1822	1822	1822	1822	1822	1822	1822	1822	1822	1822	1822	1822

PDB annotation	BINDING PROTEIN, CYTOKINE INCF 19	SIGNALLING PROTEIN TYPE I RECEPTOR, STNFR!; INCF 8 BINDING PROTEIN, CYTOKINE INCF 19	EXTRACELLULAR MODULE OSTEONECTIN, SPARC, SECRETED PROTEIN ACIDIC AND EXTRACELLULAR MODULE, GLYCOPROTEIN, ANTI-ADHESIVE PROTEIN, 2 COLLAGEN BINDING, SITE-DIRECTED MUTAGENESIS, GLYCOSYLATED 3 PROTEIN MODRES	COMPLEX (BLOOD COAGULATION/INHIBITOR) CHRISTMAS FACTOR; COMPLEX, INHIBITOR, HEMOPHILIA/BGF, BLOOD COAGULATION, 2 PLASMA, SERINE PROTEASE, CALCIUM- BINDING, HYDROLASE, 3	COMPLEX (BLOGBESTORY) COAGULATION/INHIBITOR) CHRISTMAS FACTOR; COMPLEX, INHIBITOR, HEMOPHILIA/EGF, BLOOD COAGULATION, 2 PLASMA, SERINE PROTEASE, CALCIUM- BINDING, HYDROLASE, 3	COMPLEX (BLOOD COAGULATION/INHIBITOR) CHRISTMAS FACTOR; COMPLEX,
Coumpound	B; INCF 5	TUMOR NECROSIS FACTOR RECEPTOR, INCF 4 CHAIN: A, B; INCF 5	BASEMENT MEMBRANE PROTEIN BM-40; CHAIN: A, B;	FACTOR IXA; CHAIN: C, L.; D- PHE-PRO-ARG; CHAIN: I;	FACTOR IXA; CHAIN: C, L.; D. PHE-PRO-ARG; CHAIN: I;	FACTOR IXA; CHAIN: C, L.,; D- PHE-PRO-ARG; CHAIN: I,
SEQFOL D score					55.26	
PMF score		-0.14	-0.19	-020		-0.20
Verify score		0.68	0.10	0.14		0.44
Psi Blast		1.5e-12	66-26	3e-23	3e-23	9e-14
END AA		155	171	179	178	123
STAR T AA		35	12	61	36	т
CHAI N ID		¥	¥	1	T	Ţ
PDB ID		Incf	Inub	lpfx	1pfx	1pfx
SEQ No:		1822	1822	1822	1822	1822

PDB annotation	INHIBITOR, HEMOPHILIA/EGF, BLOOD COAGULATION, 2 PLASMA, SERINE PROTEASE, CALCIUM- BINDING, HYDROLASE, 3 GLYCOPROTEIN	SERINE PROTEASE PRIFITOR FACTOR XA INHIBITOR; ANTISTASIN, CRYSTAL STRUCTURE, FACTOR XA INHIBITOR, 2 SERINE PROTEASE INHIBITOR, THROMBOSIS	SERINE PROTEASE INHIBITOR FACTOR XA INHIBITOR; ANTISTASIN, CRYSTAL STRUCTURE, FACTOR XA INHIBITOR, 2 SERINE PROTEASE INHIBITOR, THROMBOSIS	SERINE PROTEASE INHIBITOR FACTOR XA INHIBITOR; ANTISTASIN, CRYSTAL STRUCTURE, FACTOR XA INHIBITOR, 2 SERINE PROTEASE INHIBITOR THROMBOSIS	SERINE PROTEASE INHIBITOR FACTOR XA INHIBITOR; ANTISTASIN, CRYSTAL STRUCTURE, FACTOR XA INHIBITOR, 2 SERINE PROTEASE INHIBITOR THROMBOSIS	SERINE PROTEASE INHIBITOR FACTOR XA INHIBITOR; ANTISTASIN, CRYSTAL STRUCTURE, FACTOR XA INHIBITOR, 2 SERINE PROTEASE
Соитроива		ANTISTASIN; CHAIN: NULL;	ANTISTASIN; CHAIN: NULL;	ANTISTASIN; CHAIN: NULL;	ANTISTASIN; CHAIN: NULL;	ANTISTASIN; CHAIN: NULL;
SEQFOL D score					63.90	
PMF score		0.54	-0.06	0.11		-0.12
Verify score		0.63	0.57	0.03		0.61
Psi Blast		1.2e-18	7.5e-21	7.5e-25	7.5e-25	1.5e-18
END		134	147	176	180	117
STAR T AA		Z	£ 1	71	7.1	&
CHAI N ID		•				
PDB ID		1skz	1skz	1skz	1skz	1skz
SEQ NO:		1822	1822	1822	1822	1822

PDB annotation	INHIBITOR, THROMBOSIS			ANTI-COAGULANT ANTI- COAGULANT, PEPTIDIC	INHIBITORS, CONFORMATIONAL 2 FLEXIBILITY, SERINE PROTEASE INHIBITOR	APOPTOSIS TRAIL, DR5, COMPLEX												BLOOD COAGULATION FACTOR	STUART FACTOR; BLOOD	COAGULATION FACTOR, SERINE	PROTEINASE, EPIDERMAL 2 GROWTH FACTOR LIKE DOMAIN
Coumpound		LECTIN (AGGLUTININ) WHEAT GERM AGGLUTININ (ISOLECTIN 2) 9WGA 3	LECTIN (AGGLUTININ) WHEAT GERM AGGLUTININ (ISOLECTIN 2) 9WGA 3	HIRUSTASIN; CHAIN: NULL;		DEATH RECEPTOR 5; CHAIN:	A, B, C, G, H, I; TNF-RELATED APOPTOSIS INDUCING	LIGAND; CHAIN: D, E, F, J, K, L;	METALLOTHIONEIN CD-7	METALLOIMIONEIN-2 (ALFHA DOMAIN) (NIMRS) 1MHUA 2	METALLOTHIONEIN CD-7	METALLOTHIONEIN-2 (ALPHA	METALLOTHIONEIN CD-7	METALLOTHIONEIN-2 (ALPHA	DOMAIN) (NIMR\$) IMRTA 2	METALLOTHIONEIN CD-7	METALLOTHIONEIN-2 (ALPHA	BLOOD COAGULATION	FACTOR XA; CHAIN: L, C;		
SEQFOL D score		107.39									65.07					63.47					
PMF score			0.03	0.07		-0.12			1.00	!			1.00					0.10			
Verify score			0.57	0.23		0.07			0.40				0.49					0.34			
Psi Blast		6e-30	3e-26	4.5e-20		3e-08			9e-16		9e-16		9e-16			9e-16		7.5e-06			
END		158	160	107		107			108		108	·	108		1	108		106			
STAR T AA		2	2	50		46	-		78		78		78			78		54			
CEAI N ID		¥	Ą			¥												7			
PDB ID		9wga	9wga	1bx7		1 du 3			lmhu		1mhu		1 mrt		1	Till.		lxka			
SEQ ID NO:		1822	1822	1824		1824			1824		1824		1824	-	,	1824		1824			

ound PDB annotation	EIN SIN ISOFORM	EIN SIN ISOFORM	C (BETA); CALCIUM-BINDING PROTEIN CALB; CALCIUM++PHOSPHOLIPID BINDING PROTEIN, 2 CALCIUM-BINDING PROTE			VI; CHAIN: A; ENDOCYTOSIS/EXOCYTOSIS SYNAPTOTAGMIN, C2-DOMAIN, EXCOCYTOSIS, NEUROTRANSMITTER 2 RELEASE, ENDOCYTOSIS			
Coumpound	METALLOTHIONEIN METALLOTHIONEIN ISOFORM II 4MT2 3	METALLOTHIONEIN METALLOTHIONEIN ISOFORM II 4MT2 3	PROTEIN KINASE C (BETA); CHAIN: A, B;	PROTEIN KINASE C (BETA); CHAIN: A, B;	TRANSCRIPTION FACTOR PML; CHAIN: NULL;	SYNAPTOTAGMIN I; CHAIN: A;	SYNAPTOTAGMIN I; CHAIN: A;	CYTOSOLIC PHOSPHOLIPASE A2; CHAIN: A, B;	
SEQFOL D score		127.57			, , , , ,				
PIMF	0.15		1.00	0.90	0.13	1.00	0,98	0.01	
Verify	-0.09		0.47	0.27	0.33	0.68	0.70	0.17	100
Psi Blast	1.3e-14	1.3e-14	4.8e-42	3.2e-37	0.00075	3.2e-46	1.4e-27	1.1e-12	, , , ,
END	108	108	491	646	109	484	639	480	00,
STAR T AA	48	48	355	528	09	355	510	366	703
CHAI			∢	4		¥	A •	A	٧
PDB IJ	4m2	4mt2	1a25	1a25	lbor	Івуп	Ibyn	1cjy	loin
SEQ (NO: 1824	1824	1825	1825	1825	1825	1825	1825	1825

PDB annotation	HYDROLASE	LIPID DEGRADATION PLC-DI; PHOSPHORIC DIESTER HYDROLASE, HYDROLASE, LIPID	DEGRADATION, 2 TRANSDUCER,	CALCIUM-BINDING,	PHOSPHOLIPASE C, 3 PHOSPHOINOSTEDE CHECT	LPID DEGRADATION PLC-DI; PHOSPHORIC DIFFSTER	HYDROLASE, HYDROLASE, LIPID	DEGRADATION, 2 TRANSDUCER,	CALCIUM-BINDING,	PHOSPHOLIPASE C, 3	LIPID DEGRADATION PLC-DI:	PHOSPHORIC DIESTER	HYDROLASE, HYDROLASE, LIPID	DEGRADATION, 2 TRANSDUCER,	CALCIUM-BINDING,	PHOSPHOLIPASE C, 3	PHOSPHOINOSITIDE-SPECIFIC	ENDOCYTOSIS/EXOCYTOSIS BETA	SANDWICH, CALCIUM ION, C2	ENDOCYTOSIS/EXOCYTOSIS BETA	SANDWICH, CALCIUM ION, C2	DOMAIN	TRANSFERASE CALCIUM++,	PHOSPHOLIPID BINDING PROTEIN,	CALCIUM-BINDING 2 PROTEIN,	PHOSPHATIDYLSERINE, PROTEIN	TRANSFERASE CALCIUM++,
Coumpound		PHOSPHOINOSITIDE-SPECIFIC PHOSPHOLIPASE C, CHAIN: A, B;				PHOSPHOINOSITIDE-SPECIFIC PHOSPHOLIPASE C. CHAIN: A	B;				PHOSPHOINOSITIDE-SPECIFIC	PHOSPHOLIPASE C, CHAIN: A,	ii î					SYNAPTOTAGMIN III; CHAIN:	A ;	SYNAPTOTAGMIN III: CHAIN:	A ;		PROTEIN KINASE C, ALPHA	TYPE; CHAIN: A;			PROTEIN KINASE C, ALPHA
SEQFOL D score																				,	1,						
PMF score		0.62		·		0.12					0.58							1.00		0.46			96'0				0.31
Verify score		0.19				-0.07					0.16						1	0.47		0.24			0.33				0.38
Psi Blast		4.5e-15				6e-13					4.5e-15							3.2e-88		4.8e-33			1.3e-45				6.4e-40
END AA		467				620					467						3	649		179			494				920
STAR T AA		370				226					370						1) (ç		512			354				510
CHAI N ID		∢				∢ •					В							<.		A			∢				A
PDB ID		1djx				1djx	No.				1djx						14.			1dqv			ldsy			-	1dsy
SEQ ID NO:		1825				1825			_		1825			•	_		1001	C791		1825			1825				1825

PDB annotation		PHOSPHOLIPID BINDING PROTEIN, CALCIUM-BINDING 2 PROTEIN, PHOSPHATIDYLSERINE, PROTEIN KINASE C	METAL BINDING PROTEIN RING FINGER PROTEIN MATI; RING FINGER (CHICA)	HYDROLASE CALB DOMAIN; HYDROLASE, C2 DOMAIN, CALB	HYDROLASE CALB DOMAIN; HYDROLASE, C2 DOMAIN, CALB DOMAIN	DNA-BINDING PROTEIN V(D)J RECOMBINATION ACTIVATING PROTEIN I; RAGI, V(D)J RECOMBINATION, ANTIBODY, MAD, RING FINGER, 2 ZINC BINUCLEAR CLUSTER, ZINC FINGER, DNA-BINDING PROTEIN				TRANSPORT PROTEIN FYVE DOMAIN, ENDOSOME
Coumpound	-	TYPB; CHAIN: A;	CDK-ACTIVATING KINASE ASSEMBLY FACTOR MATI; CHAIN: A:	PHOSPHOLIPASE A2; CHAIN: NULL;	PHOSPHOLIPASE A2; CHAIN: NULL;	RAG1; CHAIN: NULL;	CALCIUM/PHOSPHOLIPID BINDING PROTEIN SYNAPTOTAGMIN I (FIRST C2 DOMAIN) (CALB) 1RSY 3	CALCIUMPHOSPHOLIPID BINDING PROTEIN SYNAPTOTAGMIN I (FIRST C2 DOMAIN) (CALB) 1RSY 3	CALCIUMPHOSPHOLIPID BINDING PROTEIN SYNAPTOTAGMIN I (FIRST C2 DOMAIN) (CALB) IRSY 3	PHOSPHATIDYLINOSITOL-3- PHOSPHATE BINDING FYVE
SEQFOL	D Score						81.61			
PMF	score		0.10	0.41	0.23	0.03		1.00	0.96	0.16
Verify	score		0.10	-0.18	0.31	0.21		0.81	0.48	0.04
Psi Blast			0.00045	1.5e-16	7.5e-17	0.003	4.8e-46	4.8e-46	1.6e-27	0.00075
END	Y.		601	480	189	109	483	482	636	16
STAR	I AA		09	373	528	40	347	355	510	09
CHAI	1		V			·				Ą
PDB	3		1825	lrlw	lriw	Imd	Irsy	Irsy	Irsy	lvfy
SEQ	ΝÖ		1825	1825	1825	1825	1825	1825	1825	1825

PDB annotation	MATURATION, INTRACELLULAR TRAFFICKING, 2 TRANSPORT PROTEIN	COMPLEX (GTP. BINDING/EFFECTOR) RAS-RELATED PROTEIN RAB3A; COMPLEX (GTP. BINDING/EFFECTOR), G PROTEIN, EFFECTOR, RABCDR, 2 SYNAPTIC EXOCYTOSIS, RAB PROTEIN, RAB3A, RABPHILIN	COMPLEX (GTP-BINDING/EFFECTOR) RAS-RELATED PROTEIN RAB3A; COMPLEX (GTP-BINDING/EFFECTOR), G PROTEIN, EFFECTOR, RABCDR, 2 SYNAPTIC EXOCYTOSIS, RAB PROTEIN, RAB3A, RABPHILIN	ENDOCYTOSIS/EXOCYTOSIS C2-DOMAINS, C2B-DOMAIN, RABPHILIN, ENDOCYTOSIS/EXOCYTOSIS	ENDOCYTOSIS/EXOCYTOSIS C2-DOMAINS, C2B-DOMAIN, RABPHILIN, ENDOCYTOSIS/EXOCYTOSIS		CALMODULIN, CALCIUM BINDING, HELIX-LOOP-HELIX, SIGNALLING, 2 COMPLEX(CALCIUM-BINDING PROTEINPEPTIDE)
Coumpound	CHAIN: A;	RAB-3A; CHAIN: A; RABPHILIN-3A; CHAIN: B;	RABPHILIN-3A; CHAIN: B;	RABPHILIN 3-A; CHAIN: A;	RABPHILIN 3-A; CHAIN: A;	CALCIUM-BINDING PROTEIN CALMODULIN (VERTEBRATE) ICLL 3	CALMODULIN; CHAIN: A; RS20; CHAIN: B;
SEQFOL D score			71.27		184.	69.53	72.01
PMF		0.69		1.00	0.58		
Verify score		0.40		0.62	0.53		
Psi Blast		3e-22	3e-22	3.2e-29	1.4e-46	4.8e-53	1.1e-60
END		120	131	496	649	169	170
STAR T AA		01	σò	357	512	29	26
CHAI N ID		М	A	Ą	4		A
PDB ID		1zbd	1zbd	Зтрь	3rpb	1cll	lvrk
SEQ ID NO:	- '	1825	1825	1825	1825	1828	1828

	.,				
PDB annotation	COMPLEX (BLOOD COAGULATION/INHIBITOR) AUTOPROTHROMBIN IIA; HYDROLASE, SERINE PROTEINASE), PLASMA CALCIUM BINDING, 2 GLYCOPROTEIN, COMPLEX (BLOOD COAGULATION/INHIBITOR)	COMPLEX (BLOOD COAGULATION/INHIBITOR) AUTOPROTHROMBIN IIA; HYDROLASE, SERINE PROTEINASE), PLASMA CALCIUM BINDING, 2 GLYCOPROTEIN, COMPLEX (BLOOD COAGULATION/INHIBITOR)	BLOOD COAGULATION, SERINE PROTEASE, COMPLEX, CO-FACTOR, 2 RECEPTOR ENZYME, INHIBITOR, GLA, EGF, 3 COMPLEX (SERINE PROTEASE/COFACTOR/LIGAND)	BLOOD COAGULATION, SERINE PROTEASE, COMPLEY, CO-FACTOR, 2 RECEPTOR ENZYME, INHIBITOR, GLA, EGF, 3 COMPLEX (SERINE PROTEASE/COFACTOR/LIGAND)	HYDROLASE/HYDROLASE INHIBITOR PROTEIN-PEPTIDE COMPLEX
Coumpound	ACTIVATED PROTEIN C; CHAIN: C, L; D-PHE-PRO-MAI; CHAIN: P;	ACTIVATED PROTEIN C; CHAIN: C, L; D-PHE-PRO-MAI; CHAIN: P;	BLOOD COAGULATION FACTOR VIIA; CHAIN; L, H; SOLUBLE TISSUE FACTOR; CHAIN; T, U; D-PHE-PHE-ARG- CHLOROMETHYLKETONE (DFFRCMK) WITH CHAIN; C;	BLOOD COAGULATION FACTOR VIIA; CHAIN: L, H; SOLUBLE TISSUE FACTOR; CHAIN: T, U; D-PHE-PHE-ARG. CHLOROMETHYLKETONE (DFFRCMK) WITH CHAIN: C;	DES-GLA FACTOR VIIA (HEAVY CHAIN); CHAIN: H, I; DES-GLA FACTOR VIIA (LIGHT CHAIN); CHAIN: L, M; (DPN)- PHE-ARG; CHAIN: C, D; PEPTIDE E-76; CHAIN: X, Y;
SEQFOL D score	58.73			60.57	
PMF score		-0.17	0.96		66.0
Verify score		0.14	0.10		0.26
Psi Blast	1.3e-20	1.3e-20	6.4e-16	1.5e-22	6.46-16
END	145	202	231	193	231
STAR T AA	47	73	152	54	152
CHAI N ID	,	7	1	6	ı
PDB ID	laut	laut		Idan	1dva
SEQ ID NO:	1833	1833	1833	1833	1833

PDB annotation	MATRIX PROTEIN EXTRACELLULAR MATRIX, CALCIUM-BINDING, GL YCOPROTEIN, 2 REPEAT, SIGNAL, MULTIGENE FAMILY, DISPASE MITTATION 3 FOR 1 INF	DOMAIN THOUSE, SET THE DOMAIN THOUSEN THE FRAGMENT, MATRIX PROTEIN SIGNALLING PROTEIN BINDING PROTEIN, CYTOKINE, SIGNALLING	BLOOD CLOTTING COMPLEX(SERINE PROTEASE/COFACTOR/LIGAND), BLOOD COAGULATION, 2 SERINE PROTEASE, COMPLEX, CO-FACTOR, RECEPTOR ENZYME, 3 INHIBITOR,	GLA, EGF, COMPLEX (SERINE 4 PROTEASE/COFACTORLIGAND), BLOOD CLOTTING GLYCOPROTEIN GLYCOPROTEIN GLYCOPROTEIN GLYCOPROTEIN	GLYCOPROTEIN GLYCOPROTEIN COMPLEX (BLOOD COAGULATION/INHIBITOR) CHRISTMAS FACTOR; COMPLEX, INHIBITOR, HEMOPHILIA/EGF, BLOOD COAGULATION, 2 PLASMA, SERNE PROTEASE, CALCIUM- BINDING, HYDROLASE, 3	COMPLEX (BLOOD COAGULATION/INHIBITOR) CHRISTMAS FACTOR; COMPLEX,
Coumpound	FIBRILLIN; CHAIN; NULL;	TUMOR NECROSIS FACTOR RECEPTOR; CHAIN: A, B;	BLOOD COAGULATION FACTOR VIIA; CHAIN: L; BLOOD COAGULATION FACTOR VIIA; CHAIN: H; SOLUBLE TISSUE FACTOR; CHAIN: T; 5L15; CHAIN: I;	LAMININ; CHAIN: NULL; LAMININ; CHAIN: NULL;	LAMININ; CHAIN; NULL; FACTOR IXA; CHAIN; C, L.; D. PHE-PRO-ARG; CHAIN; I;	FACTOR IXA; CHAIN: C, L.; D- PHE-PRO-ARG; CHAIN: I;
SEQFOL D score	56.72	54.06			64.61	
PMF score		4	1.00	0.43		-0.12
Verify score			0.44	0.32 0.12		0.10
Psi Blast	1.3e-15	9e-14	6,4e-16	le-28 1.1e-20	1e-28 6e-35	6e-35
END AA	226	173	231	205	146	218
STAR T AA	149	10	152	43	22	54
CEAI N ID		Ą	-		H	Li Li
PDB ID	lemn	lext	Ifak	1klo	Ppg Agd	1pfx
SEQ ID NO:	1833	1833	1833	1833	1833	1833

PDB annotation		INHIBITOR, HEMOPHILIA/EGF, BLOOD COAGULATION, 2 PLASMA, SERINE PROTEASE, CALCIUM- BINDING, HYDROLASE, 3 GLYCOPROTEINS	COMPLEX (BLOOD COAGULATION/INHIBITOR)	CHRIS I MAS FACTOR; CUMPLEX, INHIBITOR, HEMOPHILIA/EGF, BLOOD COAGITATION 2 PLASMA	SERINE PROTEASE, CALCIUM- BINDING, HYDROLASE, 3	SERINE PROTEASE FVIIA: FVIIA:	BLOOD COAGULATION, SERINE PROTEASE			SERINE PROTEASE FVIIA; FVIIA; BLOOD COAGULATION, SERINE	PROTEASE	atro:		SERINE PROTEASE FVIIA; FVIIA;	PROTEASE			SERINE PROTEASE FVIIA; FVIIA;	BLOOD COAGULATION, SERINE PROTEASE
Coumpound			FACTOR IXA; CHAIN: C, L,; D- PHE-PRO-ARG; CHAIN: I;			COAGULATION FACTOR VIIA	(LIGHT CHAIN); CHAIN: L; COAGULATION FACTOR VIIA	(HEAVY CHAIN); CHAIN: H; TRIPEPTIDYL INHIBITOR;	CHAIN: C;	COAGULATION FACTOR VIIA (LIGHT CHAIN); CHAIN: L;	COAGULATION FACTOR VIIA	(HEAVY CHAIN); CHAIN: H; TRIPEPTIDYL INHIBITOR;	CHAIN: C;	COAGULATION FACTOR VIIA	COAGULATION FACTOR VIIA	(HEAVY CHAIN); CHAIN: H;	TRIFEFTIDYL INHIBITOR; CHAIN: C:	COAGULATION FACTOR VIIA	(LIGHT CHAIN); CHAIN: L; COAGULATION FACTOR VIIA
SEQFOL	אחונג ח									S 5011				55.94		-			
PMF	acore.	- 1 - 1 - 1 - 1 - 1 - 1 - 1 - 1 - 1 - 1	0.07			0.62				0.98								0.18	
Verify	a rone		-0.16		•	0.07				0.30								0.04	
Psi Blast	. ,		6e-29	CD-JEFN -		1.5e-21				6.4e-15				7.5e-24			***	7.5e-24	
END	5		226			226				231				195				207	
STAR		-	92			156				156				16				92	
CHAI N ID			♣			L				ن				<u> </u>				rai.	
PDB			1pfx			1 g k	···		7	<u>1</u>				<u>-</u>				1qfk	
SEQ ID	ö		1833			1833				1833		.,,		1833				1833	

PDB annotation		PLASMINOGEN ACTIVATION	PLASMINOGEN ACTIVATION	PLASMINOGEN ACTIVATION	LIPID DEGRADATION PHOSPHOLIPASE A2, LIPID DEGRADATION HYDROI ASE	BLOOD COAGULATION FACTOR STUART FACTOR, BLOOD COAGULATION FACTOR, SERINE PROTEINASE, EPIDERMAL 2 GROWTH FACTOR LIKE DOMAIN	BLOOD COAGULATION FACTOR STUART FACTOR, BLOOD COAGULATION FACTOR, SERINE PROTEINASE, EPIDERMAL 2 GROWTH FACTOR I IKE DIOMAIN	BLOOD COAGULATION FACTOR STUART FACTOR; BLOOD COAGULATION FACTOR, SERINE PROTEINASE, EPIDERMAL 2 GROWTH FACTOR LIKE DOMAIN	
Coumpound	(HEAVY CHAIN); CHAIN: H; TRIPEPTIDYL INHIBITOR; CHAIN: C;	T-PLASMINOGEN ACTIVATOR FI-G; 1TPG 7 CHAIN: NULL; 1TPG 8	T-PLASMINOGEN ACTIVATOR FI-G; ITPG 7 CHAIN: NULL; ITPG 8	T-PLASMINOGEN ACTIVATOR FI-G; ITPG 7 CHAIN: NULL; ITPG 8	PHOSPHOLIPASE A2; CHAIN: A, B;	BLOOD COAGULATION FACTOR XA; CHAIN: L, C;	BLOOD COAGULATION FACTOR XA; CHAIN: L, C;	BLOOD COAGULATION FACTOR XA; CHAIN: L, C;	LECTIN (AGGLUTININ) WHEAT GERM AGGLUTININ (ISOLECTIN 2) 9WGA 3
SEQFOL D score							59.27		78.80
PMF		0.63	0.19	0.16	-0.12	0.64		0.06	
Verify score		-0.02	0.27	0.23	0.03	0.18		0.32	
Psi Blast		Ie-23	le-23	3e-21	4.5e-18	3e-18	1.1e-21	1.16-21	7.5e-25
END		226	125	196	130	226	208	207	207
STAR T AA		137	43	72	34	156	16	92	28
CHAI N ID					K	T	T	—	V V
PDB ID		1tpg	14pg	149g	lvap	lxka	lxka	lxka	9wga
SEQ No:		1833	1833	1833	1833	1833	1833	1833 33	1833

PDB annotation	SIGNALING PROTEIN PHOTORECEPTOR, G PROTEIN. COUPLED RECEPTOR, MEMBRANE PROTEIN, 2 RETINAL PROTEIN, VISUAL PIGMENT	SIGNALING PROTEIN PHOTORECEPTOR, G PROTEIN- COUPLED RECEPTOR, MEMBRANE PROTEIN, 2 RETINAL PROTEIN, VISUAL PIGMENT	RNA-BINDING PROTEIN/RNA TRA PRE-MRNA; SPLICING REGULATION, RNP DOMAIN, RNA COMPI EX	TRANSFERASE TYPE II DNA- (CYTOSINE N4) METHYLTRANSFERASE, AMINO 2 METHYLATION, SELENOMETHIONINE, MULTIWAVELENGTH ANOMALOUS 3 DIFFRACTION	GENE REGULATION/RNA POLY(A) BINDING PROTEIN I, PABP 1; RRM, PROTEIN-RNA COMPLEX, GENE REGULATION/RNA	GENE REGULATIONRNA POLY(A) BINDING PROTEIN 1, PABP 1; RRM, PROTEIN-RNA COMPLEX, GENE REGULATION/RNA
Coumpound	RHODOPSIN; CHAIN: A, B	RHODOPSIN; CHAIN: A, B	SXL-LETHAL PROTEIN; CHAIN: A, B; RNA (5'- R(P*GP*UP*UP*UP*UP*) UP*UP*UP*UP*). CHAIN: P.O.	N-4 CYTOSINE-SPECIFIC METHYLTRANSFERASE PVU II; CHAIN: A;	POLYDENYLATE BINDING PROTEIN I; CHAIN: A, B, C, D, E, F, G, H; RNA (5'- R(*AP*AP*AP*AP*AP*AP* AP*AP*AP*A); CHAIN: M, N, O, P, O, R, S, T;	POLYDENYLATE BINDING PROTEIN 1; CHAIN: A, B, C, D, E, F, G, H; RNA (5'- R(*AP*AP*AP*AP*AP*AP*AP* AP*AP*AP*A); CHAIN: M, N, O, P, Q, R, S, T;
SEQFOL D score	·					
PMF	-0.07	0.10	0.36	0.27	0.24	-0.19
Verify score	0.11	-0.14	-0.03	-0.57	-0.34	0.05
Psi Blast	3e-20	7.5e-18	1.6e-19	4.5e-05	6.4e-23	3.2e-26
END	320	299	144	480	150	237
STAR T AA	4	4	19	433	59	75
CHAI N ID	Ą	മ	Ą	₹	Ą	щ
PDB ID	1f88	1f88	1b7f	1600	levj	levj
SEQ ID NO:	1834	1834	1835	1835	1835	1835

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PDB annotation		TRANSFERASE METHYLTRANSFERASE	RNA BINDING PROTEIN RNA- BINDING DOMAIN	STRUCTURAL GENOMICS	HYPOTHETICAL PROTEIN, METHANOCOCCUS JANNASCHII	STRUCTURAL PROTEIN PROTEIN	C23; RNP, RBD, RRM, RNA BINDING	TRANSFERASE SAM. BINDING	DOMAIN, BETA-BARREL, MIXED	ALPHA-BETA, HEXAMER, 2 DIMER	TRANSFERASE SAM-BINDING	DOMAIN, BETA-BARREL, MIXED	ALPHA-BETA, HEXAMER, 2 DIMER	RNA BINDING PROTEIN RNA-	BINDING DOMAIN	TRANSFERASE RRNA	METHYLTRANSFERASE ERMC',	COFACTOR ANALOGS	TRANSFERASE RRNA	METHYLTRANSFERASE ERMC',	COFACTOR ANALOGS	TRANSFERASE	(METHYLTRANCEMENSE) COMT;	TRANSFERASE,	METHYL TRANSFERASE,	NEUROTRANSMITTER DEGRADATION	METHYLTRANSFERASE GNMT. S-	ADENOSYL-L-METHIONINE\;
Coumpound	•	GLYCINE N. METHYLTRANSFERASE; CHAIN: A, B, C, D;	HU ANTIGEN C; CHAIN: A;	MJ0882; CHAIN; A;		NUCLEOLIN RBD2; CHAIN: A;		HNRNP ARGININE N	METHYLTRANSFERASE;	CHAIN: 1, 2, 3, 4, 5, 6;	HNRNP ARGININE N-	METHYLTRANSFERASE;	CHAIN: 1, 2, 3, 4, 5, 6;	HETEROGENEOUS NUCLEAR	KIBONUCLEOPROTEIN DO; CHAIN: A;	ERMC'	METHYLTRANSFERASE;	CHAIN: A;	ERMC	METHYLTRANSFERASE;	CHAIN: A;	CATECHOL O.	METHYL TRANSFERASE;	CHAIN: NULL;	3 * * * * * * * * * * * * * * * * * * *		GLYCINE N.	METHYLTRANSFERASE;
SEQFOL	D score																-									-	-	
PMF	sсоте	0.17	0.16	0.75		0.62		0.03			0.83			90.0		0.58			0.05			99.0					0.05	
Verify	score	-0.57	-0.02	0.37		0.19		-0.51			0.20			0.27		-0.06	-		-0.12			0.23					-0.47	
Psi Blast		1.2e-14	3.2e-17	9.6e-20		1.3e-13		3.2e-11		,	1.3e-13		60	3.26-23		6e-21		,	6.4e-05		,	1.5e-15					1.Se-10	
END	AA	492	144	267		139	-	580			492		;	+ + + +		592			524			238					492	
STAR	TAA	424	72	421		73		402		96	420	-	i	ŧ.		410		55,	413		13	474	_				426	
CHAI	A D	∢	¥	Ą		∢'		-			-	•		ζ.		∢			€			-	-	•			A	
PDB	A	1d2h	149a	Idus		lfjc		1g6q			pog1		16.41	1501		lqam			uigh t			DIAT			***		lxva	
SEQ	ΘÖ	1835	1835	1835		1835		1835		200	1835		1025	505		1835		1005	1001		101	101					1835	

	-,								
PDB annotation	GLYCINE METHYLTRANSFERASE	RNA BINDING PROTEIN RNA- BINDING DOMAIN	RNA-BINDING DOMAIN RNA- BINDING DOMAIN, ALTERNATIVE SPLICING	RNA BINDING DOMAIN RNA BINDING DOMAIN, RBD, RNA RECOGNITION MOTIF, RRM, 2 SPLICING INHIBITOR, TRANSLATIONAL INHIBITOR, SEX 3 DETERMINATION, X CHROMOSOME DOSAGE COMPENSATION	GENE REGULATION POZ DOMAIN; PROTEIN-PROTEIN INTERACTION DOMAIN, TRANSCRIPTIONAL 2 REPRESSOR, ZINC-FINGER PROTEIN, X-RA Y CRYSTALLOGRAPHY, 3 PROTEIN STRUCTURE, PROMYELOCYTIC LEUKEMIA, GENE REGULATION				BLOOD COAGULATION, SERINE PROTEASE, COMPLEX, CO-FACTOR.
Coumpound	CHAIN: A, B;	MUSASHII; CHAIN: A;	SEX-LETHAL PROTEIN; CHAIN: NULL;	SEX-LETHAL; CHAIN: A, B, C;	PROMYELOCYTIC LEUKEMIA ZINC FINGER PROTEIN PLZF; CHAIN: A;	OXIDOREDUCTASE(OXYGEN(A)) GALACTOSE OXIDASE (E.C.1.1.3.9) (PH 4.5) 1GOF 3	OXIDOREDUCTASE(OXYGEN(A)) GALACTOSE OXIDASE (E.C.1.1.3.9) (PH 4.5) IGOF 3	OXIDOREDUCTASE(OXYGEN(A)) GALACTOSE OXIDASE (E.C.1.1.3.9) (PH 4.5) 1GOF 3	BLOOD COAGULATION FACTOR VIIA; CHAIN: L, H;
SEQFOL D score					·				
PMF		0.00	0.35	-0.05	-0.05	0.34	0.13	0.07	-0.20
Verify score		-0.04	0.04	0.10	0.37	-0.33	-0.42	-0.23	-0.00
Psi Blast		4.8e-18	8e-18	86-18	3.2e-16	1.6e-06	7.5e-13	1.5e-15	4.8e-10
END		144	152	137	85	505	450	372	370
STAR T AA		74	57	61	4	204	217	246	285
CHAI N ID		¥	~ ~~	Ą	∢ •				ม
PDB ID		2mss	2sx1	3sxI	lbuo	lgof	lgof	1gof	Idan
SEQ ID NO:		1835	1835	1835	98	1836	1836	1836	1837

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otation		ME, INHIBITOR,	EX (SERINE	FOR/LIGAND)		TON, SERINE	EX, CO-FACTOR,	ME, INHIBITOR,	EX (SERIME	(DIK/LIGAND)	•	TON, SERINE	EX, CO-FACTOR,	ME, INHIBITOR,	EX (SERINE	TOR/LIGAND)		OLASE	N-PEPTIDE					OLASE	N-PEPTIDE					OLASE	V-PEPTIDE				
PDB annotation		2 RECEPTOR ENZYME, INHIBITOR,	GLA, EGF, 3 COMPLEX (SERINE	PROTEASE/COFACTOR/LIGAND)		BLOOD COAGULATION, SERINE	PROTEASE, COMPLEX, CO-FACTOR,	2 RECEPTOR ENZYME, INHIBITOR,	GLA, EGF, 3 COMPI	PROTEASE/COFACTOR/LIGAND)		BLOOD COAGULATION, SERINE	PROTEASE, COMPLEX, CO-FACTOR.	2 RECEPTOR ENZYME, INHIBITOR,	GLA, EGF, 3 COMPLEX (SERINE	PROTEASE/COFACTOR/LIGAND)		HYDROLASE/HYDROLASE	INHIBITOR PROTEIN-PEPTIDE	COMPLEX				HYDROLASE/HYDROLASE	INHIBITOR PROTEIN-PEPTIDE	COMPLEX				HYDROLASE/HYDROLASE	INHIBITOR PROTEIN-PEPTIDE	COMPLEX			
Coumpound		SOLUBLE TISSUE FACTOR;	CHAIN: T, U; D-PHE-PHE-ARG-	CHLOROMETHYLKETONE	(DFFRCMK) WITH CHAIN: C;	BLOOD COAGULATION	FACTOR VIIA; CHAIN: L, H;	SOLUBLE TISSUE FACTOR;	CHAIN: T, U; D-PHE-PHE-ARG-	CHLOROMETHYLKETONE	(DFFRCMK) WITH CHAIN: C;	BLOOD COAGULATION	FACTOR VIIA; CHAIN: L, H;	SOLUBLE TISSUE FACTOR;	CHAIN: T, U; D-PHE-PHE-ARG.	CHLOROMETHYLKETONE	(DFFRCMK) WITH CHAIN: C;	DES-GLA FACTOR VIIA	(HEAVY CHAIN); CHAIN: H, I;	DES-GLA FACTOR VIIA (LIGHT	CHAIN); CHAIN; L, M; (DPN)-	PHE-ARG; CHAIN: C, D;	PEPTIDE E-76; CHAIN: X, Y;	DES-GLA FACTOR VIIA	(HEAVY CHAIN); CHAIN: H, I;	DES-GLA FACTOR VIIA (LIGHT	CHAIN); CHAIN: L, M; (DPN)-	PHE-ARG; CHAIN: C, D;	PEPTIDE E-76; CHAIN: X, Y;	DES-GLA FACTOR VIIA	(HEAVY CHAIN); CHAIN: H, I;	DES-GLA FACTOR VIIA (LIGHT	CHAIN); CHAIN: L', M; (DPN)-	PHE-ARG: CHAIN: C. D.	
SEQFOL	a rone or		-					-					-		<u>-</u>							_	1			_	_		144	1				_	•
PMF	21025					979						-0.20		,				-0.20						-0.19						-0.20			-		
Verify	31335	-				0.04				_		0.21						0.09						0.10				_		0.27					
Psi Blast					,	1.le-12						3.2e-08						4.8e-10						I.1e-12						3.2e-08			d Barrier		
END						449						583	-					370						1						583					
STAR						361						530						285						361						230				_	
CHAI N ID		_				- -}										-				_				ب ا						<u>-</u>					
PDB TD			-			Iden		-				ldan						ldva						Idva			-	••		ldva		•			
SEQ	NO:				1001	1837						1837						1837						1837						1837				_	•

PDB annotation	MATRIX PROTEIN EXTRACELLULAR MATRIX, CALCIUM-BINDING, GLYCOPROTEIN, 2 REPEAT, SIGNAL, MULTIGENE FAMILY, DISEASE MUTATION, 3 EGF-LIKE DOMAIN, HUMAN FIBRILLIN-1 FRAGMENT, MATRIX PROTEIN	MATRIX PROTEIN EXTRACELLULAR MATRIX, CALCIUM-BINDING, GLYCOPROTEIN, 2 REPEAT, SIGNAL, MULTIGENE FAMILY, DISEASE MUTATION, 3 EGF-LIKE DOMAIN, HUMAN FIBRILLIN-1 FRAGMENT, MATRIX PROTEIN	MATRIX PROTEIN EXTRACELLULAR MATRIX, CALCIUM-BINDING, GLYCOPROTEIN, 2 REPEAT, SIGNAL, MULTIGENE FAMILY, DISEASE MUTATION, 3 EGF-LIKE DOMAIN, HUMAN FIBRILLIN-1 FRAGMENT, MATRIX PROTEIN	LIPID BINDING PROTEIN LDL RECEPTOR; BETA HAIRPIN, 3-10 HELIX, CALCIUM BINDING	LIPID BINDING PROTEIN LDL RECEPTOR; BETA HAIRPIN, 3-10 HELIX, CALCIUM BINDING	BLOOD CLOTTING COMPLEX(SERINE PROTEASE/COFACTOR/LIGAND), BLOOD COAGULATION, 2 SERINE
Соитроинд	FIBRILLIN; CHAIN: NULL;	FIBRILLIN; CHAIN: NULL;	FIBRILLIN; CHAIN: NULL;	LOW-DENSITY LIPOPROTEIN RECEPTOR; CHAIN: A;	LOW-DENSITY LIPOPROTEIN RECEPTOR; CHAIN: A;	BLOOD COAGULATION FACTOR VIIA; CHAIN: L; BLOOD COAGULATION FACTOR VIIA; CHAIN: H;
SEQFOL D score						
PMF score	-0.19	-0.17	-0.20	-0.20	-0.20	-0.20
Verify score	0.19	0.07	0.03	0.03	0.13	0.22
Psi Blast	1.4e-10	3.2e-09	4.8e-09	1.6e-11	4.8e-09	3.2e-08
END AA	285	227	283	182	221	583
STAR T AA	107	149	530	102	143	530
CHAI N ID	•			A	∢	L)
PDB ID	lemo	lemn	lemn	1f5y	1f5y	lfak
SEQ NO:	1837	1837	1837	1837	1837	1837

CHAI N ID	STAR T AA	END AA	Psi Blast	Verify score	PMF	SEQFOL D score	Coumpound	PDB annotation
. 1.							SOLUBLE TISSUE FACTOR; CHAIN: T; 5L15; CHAIN: I;	PROTEASE, COMPLEX, CO-FACTOR, RECEPTOR ENZYME, 3 INHIBITOR, GLA, EGF, COMPLEX (SERINE 4 PROTEASE/COFACTOR/LIGAND), BI OOD CLOTTING
	328	409	1.1e-12	0.22	-0.13	:	FACTOR IXA; CHAIN: C, L,; D. PHE-PRO-ARG; CHAIN: I;	COMPLEX (BLOOD COAGULATION/INHIBITOR) CHRISTMAS FACTOR; COMPLEX, INHIBITOR, HEMOPHILIA/EGF, BLOOD COAGULATION, 2 PLASMA, SERINE PROTEASE, CALCIUM- BINDING, HYDROLASE, 3
I	361	449	1.6e-11	0.16	-0.19		FACTOR IXA; CHAIN: C, L,; D- PHE-PRO-ARG; CHAIN: I;	COMPLEX (BLOOD COAGULATION/MHIBITOR) CHRISTMAS FACTOR; COMPLEX, NHIBITOR, HEMOPHILIA/EGF, BLOOD COAGULATION, 2 PLASMA, SERINE PROTEASE, CALCIUM- BINDING, HYDROLASE, 3
	152	243	4.8e-10	0.03	-0.15		COAGULATION FACTOR VIIA (LIGHT CHAIN); CHAIN: L; COAGULATION FACTOR VIIA (HEAVY CHAIN); CHAIN: H; TRIPEPTIDYL INHIBITOR; CHAIN: C;	SERINE PROTEASE FVIIA; FVIIA; BLOOD COAGULATION, SERINE PROTEASE
	365	449	6.4e-12	0.02	-0.19		COAGULATION FACTOR VIIA (LIGHT CHAIN); CHAIN: L; COAGULATION FACTOR VIIA (HEAVY CHAIN); CHAIN: H; TRIPEPTIDYL INHIBITOR;	SERINE PROTEASE FVIIA; BLOOD COAGULATION, SERINE PROTEASE
	530	583	3.2e-08	0.08	-0.20		COAGULATION FACTOR VIIA	SERINE PROTEASE FVIIA; FVIIA;

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PDB annotation	BLOOD COAGULATION, SERINE PROTEASE		BLOOD COAGULATION FACTOR STUART FACTOR; BLOOD COAGULATION FACTOR, SERINE PROTEINASE, EPIDERMAL 2 GROWTH FACTOR LIKE DOMAIN	BLOOD COAGULATION FACTOR STUART FACTOR; BLOOD COAGULATION FACTOR, SERINE PROTEINASE, EPIDERMAL 2 GROWTH FACTOR LIKE DOMAIN			HYDROLASE HYDROLASE, NAD BINDING PROTEIN	OXIDOREDUCTASE OXIDOREDUCTASE_TROPANE ALKALOID BIOSYNTHESIS, REDUCTION OF 2 TROPINONE TO TROPINE, SHORT-CHAIN DEHYDROGENASE
Coumpound	(LIGHT CHAIN); CHAIN: L; COAGULATION FACTOR VIIA (HEAVY CHAIN); CHAIN: H; TRIPEPTIDYL INHIBITOR; CHAIN: C;	MEMBRANE PROTEIN VITELLINE MEMBRANE OUTER LAYER PROTEIN I IVMO 3	BLOOD COAGULATION FACTOR XA; CHAIN: L, C;	BLOOD COAGULATION FACTOR XA; CHAIN: L, C;	LECTIN (AGGLUTININ) WHEAT GERM AGGLUTININ (ISOLECTIN 2) 9WGA 3	LECTIN (AGGLUTININ) WHEAT GERM AGGLUTININ (ISOLECTIN 2) 9WGA 3	S-ADENOSYLHOMOCYSTEINE HYDROLASE; CHAIN: A, B;	TROPINONE REDUCTASE-1; CHAIN: A, B;
SEQFOL D score						,		
PMF score		-0.19	-0.20	-0.20	-0.14	-0.14	0.00	0.21
Verify score		0.19	0.22	0.04	0.21	0.01	-0.09	0.34
Psi Blast		3e-15	1.6e-08	4.8e-11	9.6e-16	4.8e-16	0.0032	0.00064
END		470	585	158	403	476	207	215
STAR T AA		303	530	73	250	275	163	173
CHAI N ID		Ą	니	μÌ	Ą	A	А	◆
PDB CI		lvmo	Lxka	Ixka	9м8а	9мда	1a7a	lae]
SEQ NO EQ		1837	1837	1837	1837	1837	1838	1838

		·	,		**********	· 1900			Appendix and week
PDB annotation	OXIDOREDUCTASE OXIDOREDUCTASE, TROPANE ALKALOID BIOSYNTHESIS, REDUCTION OF 2 TROPINONE TO TROPINE, SHORT-CHAIN DEHYDROGENASE	OXIDOREDUCTASE NAD- DEPENDENT OXIDOREDUCTASE, SHORT-CHAIN ALCOHOL 2 DEHYDROGENASE, PCB DEGRADATION	OXIDOREDUCTASE AMINO ACID DEHYDROGENASE, OXIDATIVE DEAMINATION MECHANISM, 2 OXIDOREDUCTASE	OXIDOREDUCTASE (CH-OH(D)- NAD(A)) OXIDOREDUCTASE 1CDO 15	OXIDOREDUCTASE (CH-OH(D)- NAD(A)) OXIDOREDUCTASE 1ÇDO 15	OXIDOREDUCTASE SHORT-CHAIN DEHYDROGENASE, OXIDOREDUCTASE	OXIDOREDUCTASE RETINOL DEHYDROGENASE, GASTRIC ALCOHOL ROSSMANN OR DINUCLEOTIDE FOLD	OXIDOREDUCTASE RETINOL DEHYDROGENASE, GASTRIC ALCOHOL ROSSMANN OR DINUCLEOTIDE FOLD	OXIDOREDUCTASE BETA! ADH; IDEH 9 NAD+ DEPENDENT
Coumpound	TROPINONE REDUCTASE-I; CHAIN: A, B;	CIS-BIPHENYL-2,3- DIHYDRODIOL-2,3- DEHYDROGENASE; CHAIN: NULL;	L-PHENYLALANINE DEHYDROGENASE; CHAIN: A; L-PHENYLALANINE DEHYDROGENASE; CHAIN: B;	ALCOHOL DEHYDROGENASE; ICDO 6 CHAIN: A, B; 1CDO 7	ALCOHOL DEHYDROGENASE; 1CDO 6 CHAIN: A, B; 1CDO 7	CARBONYL REDUCTASE; CHAIN: A, B, C, D;	ALCOHOL DEHYDROGENASE CLASS IV SIGMA CHAIN; CHAIN: A, B, C, D;	ALCOHOL DEHYDROGENASE CLASS IV SIGMA CHAIN; CHAIN: A, B, C, D;	HUMAN BETA! ALCOHOL DEHYDROGENASE; IDEH 7
SEQFOL D score	. ,			56.21			64.19		
PMF score	0.05	0.25	0.89		1.00	0.03		1.00	1.00
Verify score	0.44	-0.07	0.67		0.64	0.19		0.81	0.63
Psi Blast	0.00064	4.8e-05	0.00013	1.3e-76	1.3e-76	3.2e-05	4,8e-75	4.8e-75	3.2e-81
END AA	215	222	221	367	366	261	367	366	366
STAR T AA	173		173		25	173	1	26	25
CHAI N ID	В		∢;	A	A	• •	Ą	Ą	¥
FDB CI	1ae1	1bdb	p cld	Icdo	1cdo	lcyd	Idit	ldlt	l deh
SEQ ID NO:	1838	1838	1838	1838	1838	1838	1838	18 38	1838

PDB annotation	ALCOHOL DEHYDROGENASE 1DEH	OXIDOREDUCTASE BETA! ADH; IDEH 9 NAD+ DEPENDENT ALCOHOL DEHYDROGENASE IDEH 26			•	OXIDOREDUCTASE OXIDOREDUCTASE, ZINC, NADP	OXIDOREDUCTASE OXIDOREDUCTASE, ZINC, NADP	OXIDOREDUCTASE OXIDOREDUCTASE		
Coumpound	CHAIN: A, B; 1DEH 8	HUMAN BETA1 ALCOHOL DEHYDROGENASE; 1DEH 7 CHAIN: A, B; 1DEH 8	ALCOHOL DEHYDROGENASE, CLASS II; CHAIN: A, B;	ALCOHOL DEHYDROGENASE; CHAIN: A, B;	OXIDOREDUCTASE 3-ALPHA, 20-BETA-HYDROXYSTEROID DEHYDROGENASE (E.C.1.1.1.53) 1HDC 3 COMPLEXED WITH CARRENOXOLONE 1HDC 4	NADP-DEPENDENT ALCOHOL DEHYDROGENASE; CHAIN: A, B, C, D;	NADP-DEPENDENT ALCOHOL DEHYDROGENASE; CHAIN: A, B, C, D;	FLAVOCYTOCHROME C3 FUMARATE REDUCTASE; CHAIN: A, D;	OXIDOREDUCTASE QUINONE OXIDOREDUCTASE COMPLEXED WITH NADPH 10OR 3	OXIDOREDUCTASE QUINONE OXIDOREDUCTASE
SEQFOL D score		74.95				53.09		·	116.09	
PMF score			1.00	1:00	0.45		1.00	0.47		1.00
Verify score			0.77	0.73	-0.03		0.59	0.28		0.75
Psi Blast		3.2e-81	1.6e-69	4.8e-77	9.6e-07	1.6e-51	1.6e-51	0.0032	8e-70	8e-70
END AA		367	366	366	284	369	367	207	370	367
STAR T AA		ဇာ	26	25	173	24	50	168	37	38
CHAI N ID		∢	¥	¥	∢ • .	4	A	A	Ą	٧
PDB ID		ldeh	le3i	lee2	1hdc	1kev	Ikev	1908	lqor	Iqor
SEQ ID NO:		1838	1838	1838	1838	1838	1838	1838	1838	1838

SEQ EL SE	80g 11	CHAI N ID	STAR T AA	END	Psi Blast	Verify score	PMF score	SEQFOL D score	Coumpound	PDB annotation
									100R 3	
183	Iteh	◆	-	367	1.6e-86			72.11	HUMAN CHICHI ALCOHOL DEHYDROGENASE; CHAIN: A, B;	OXIDOREDUCTASE GLUTATHIONE- DEPENDENT FORMALDEHYDE DEHYDROGENASE, NAD+ DEPENDENT ALCOHOL DEHYDROGENASE 2 GLUTATHIONE DEPENDENT FORMALDEHYDE DEHYDROGENASE
80 33 33 80 80 80 80 80 80 80 80 80 80 80 80 80	Iteh	A	27	366	1.6e-86	0.60	1.00		HUMAN CHICHI ALCOHOL DEHYDROGENASE; CHAIN: A, B;	OXIDOREDUCTASE GLUTATHIONE. DEPENDENT FORMALDEHYDE DEHYDROGENASE, NAD+ DEPENDENT ALCOHOL DEHYDROGENASE 2 GLUTATHIONE DEPENDENT FORMALDEHYDE DEHYDROGENASE
1838	lvid		164	268	60000	0.51	0.47		CATECHOL O- METHYLTRANSFERASE; CHAIN: NULL;	TRANSFERASE (METHYLTRANSFERASE) COMT; TRANSFERASE, METHYLTRANSFERASE, NEUROTRANSMITTER DEGRADATION
1838	lybv	A	173	280	9.6e-05	-0.20	0.49		TRIHYDROXYNAPHTHALENE REDUCTASE; CHAIN: A, B;	OXIDOREDUCTASE NAPHTHOL REDUCTASE: OXIDOREDUCTASE
1838	lykf	Ą	24	370	4.8e-54			52.30	NADP-DEPENDENT ALCOHOL DEHYDROGENASE; CHAIN: A, B, C, D;	OXIDOREDUCTASE OXIDOREDUCTASE
1838	lykf	∢	22	367	4.8e-54	0.56	1.00		NADP-DEPENDENT ALCOHOL DEHYDROGENASE; CHAIN: A, B, C, D;	OXIDOREDUCTASE OXIDOREDUCTASE
1839	1a06		71	349	9,6e-09			52.68	CALCIUM/CALMODULIN. DEPENDENT PROTEIN KINASE;	KINASE KINASE, SIGNAL TRANSDUCTION,

PDB annotation	CALCIUM/CALMODULIN	COMPLEX (ISOMERASE/PROTEIN	KINASE) FKBP12;	SERINE/THREONINE-PROTEIN	KINASE RECEPTOR R4; COMPLEX	(ISOMERASE/PROTEIN KINASE),	RECEPTOR 2 SERINE/THREONINE	KINASE	COMPLEX (ISOMERASE/PROTEIN	KINASE) FKBP12;	SERINE/THREONINE-PROTEIN	KINASE RECEPTOR R4; COMPLEX	(ISOMERASE/PROTEIN KINASE),	RECEPTOR 2 SERINE/THREONINE	KINASE	TRANSFERASE CSK; PROTEIN	KINASE, C-TERMINAL SRC KINASE,	PHOSPHORYLATION, 2	STAUROSPORINE, TRANSFERASE	TRANSFERASE CSK; PROTEIN	KINASE, C-TERMINAL SRC KINASE,	PHOSPHORYLATION, 2	STAUROSPORINE, TRANSFERASE	TRANSFERASE CSK; PROTEIN	KINASE, C-TERMINAL SRC KINASE,	PHOSPHORYLATION, 2	STAUROSPORINE, TRANSFERASE	PHOSPHOTRANSFERASE FGFRIK,	FIBROBLAST GROWTH FACTOR	RECEPTOR 1; TRANSFERASE,	TYROSINE-PROTEIN KINASE, ATP-	BINDING, 2 PHOSPHORYLATION,	RECEPTOR, PHOSPHOTRANSFERASE
Coumpound	CHAIN: NULL;	FK506-BINDING PROTEIN;	CHAIN: A, C, E, G; TGF-B	SUPERFAMILY RECEPTOR	TYPE I; CHAIN: B, D, F, H;				FK506-BINDING PROTEIN;	CHAIN: A, C, E, G; TGF-B	SUPERFAMILY RECEPTOR	TYPE I; CHAIN: B, D, F, H;				C-TERMINAL SRC KINASE;	CHAIN: A;			C-TERMINAL SRC KINASE;	CHAIN: A;			C-TERMINAL SRC KINASE;	CHAIN: A;			FGF RECEPTOR 1; CHAIN: A, B;					
SEQFOL D score		58.79							_							62.45												70.22					
PMT score									90.0											0.00				0.01									
Verify score									-0.17											-0.33				-0.39									
Psi Blast		1.1e-15							1.5e-13							3.2e-27				I.5e-13				3.2e-27				1.1e-26				•	
END AA		350	_						199							337				197				334				339					
STAR T AA		20							₽					-		73				%				87				8					
CHAI N ID		В							æ							₩				∢				₹				₩					
PDB ID		1566						7	1566						7	lbyg			-+	1byg	-	-		lbyg				lîgk				,	
SEQ ID NO:		1839							1839					,		1839				1839		-		1839				1839					

PDB annotation	PHOSPHOTRANSFERASE FGFRIK, FIBROBLAST GROWTH FACTOR RECEPTOR 1; TRANSFERASE, TYROSINE-PROTEIN KINASE, ATP-BINDING, 2 PHOSPHORYLATION, RECEPTOR, PHOSPHOTRANSFERASE	PHOSPHOTRANSFERASE FGFR1K, FIBROBLAST GROWTH FACTOR RECEPTOR 1; TRANSFERASE, TYROSINE-PROTEIN KINASE, ATP- BINDING, 2 PHOSPHORYLATION, RECEPTOR,	TRANSFERASE P150, C-ABL; KINASE, KINASE INHIBITOR, STI- 571, ACTIVATION LOOP	PROTEIN KINASE CDK2; TRANSFERASE, SERINE/THREONINE PROTEIN KINASE, ATP-BINDING, 2 CELL CYCLE, CELL DIVISION, MITOSIS, PHOSPHORYLATION	COMPLEX (TRANSFERASE/SUBSTRATE) TYROSINE KINASE, SIGNAL TRANSDUCTION, PHOSPHOTRANSFERASE, 2 COMPLEX (KINASE/PEPTIDE SUBSTRATE/ATP ANALOG), ENZYME, 3 COMPLEX (TRANSFERASE/SUBSTRATE)	COMPLEX (TRANSFERASE/SUBSTRATE)
Coumpound	FGF RECEPTOR 1; CHAIN: A, B;	FGF RECEPTOR I; CHAIN: A, B;	PROTO-ONCOGENE TYROSINE-PROTEIN KINASE ABL; CHAIN: A, B;		INSULIN RECEPTOR; CHAIN: A; PEPTIDE SUBSTRATE; CHAIN: B;	INSULIN RECEPTOR; CHAIN: A; PEPTIDE SUBSTRATE; CHAIN:
SEQFOL D score	71.37	: :		:	61.82	
PMF score		0.41	0.10	0.33		0.16
Verify score		0.11	-0.20	-0.13		0.10
Psi Blast	3.2e-26	3.26-26	1.6e-27	1.4e-22	3.2e-26	3.2e-26
END AA	338	335	332	321	350	332
STAR T AA	63	87	84	79	63	87
CHAI N ID	æ	æ	∢		Ą	¥
PDB ID	1fgk	1fgk	1fpu	lhcl	1ir3	1ir3
) E E	1839	939	1839	1839	1839	1839

CHAI	J STAR TAA	AA AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Coumpound	PDB annotation
1							j,	TYROSINE KINASE, SIGNAL TRANSDUCTION, PHOSPHOTRANSFERASE, 2
		·						COMPLEX (KINASE/PEPTIDE SUBSTRATE/ATP ANALOG),
						***********		ENZYME, 3 COMPLEX (TRANSFERASE/SUBSTRATE)
I	84	347	1.1e-24	-0.26	0.29		HAEMATOPOETIC CELL KINASE (HCK); CHAIN: A;	TYROSINE KINASE TYROSINE KINASE-INHIBITOR COMPLEX,
								DOWN-REGULATED KINASE, 2 ORDERED ACTIVATION LOOP
	.83	336	1.6e-20	-0.38	0.03		VASCULAR ENDOTHELIAL GROWTH FACTOR RECEPTOR CHAIN: A;	TRANSFERASE KDR; TYROSINE KINASE
	7	176	8e-09	0.14	-0.20		TROPOMYOSIN; CHAIN: A, B,	CONTRACTILE PROTEIN TROPOMYOSIN COIL ED-COIL
								ALPHA-HELICAL, CONTRACTILE PROTEIN
	62	164	1.3e-08	0.19	-0.13		METHYLMALONYL-COA MUTASE: CHAIN: A. B. C. D:	ISOMERASE ISOMERASE, MUTASE, INTRAMOLECULAR TRANSFERASE
İ	9	112	4.5e-09	0.53	-0.19		TRANSDUCIN; CHAIN: B, G;	COMPLEX
		······································					PHOSDUCIN; CHAIN: P;	(TRANSDUCER/TRANSDUCTION) GT BETA-GAMMA: MEKA, PP33:
					-			PHOSDUCIN, TRANSDUCIN, BETA-
	. _					·		GAMMA, SIGNAL TRANSDUCTION,
							· · · · · · · · · · · · · · · · · · ·	PHOSPHORYLATION, G PROTEINS,
_								THIOREDOXIN, 3 VISION, MEKA,
- 1								(TRANSDUCER/TRANSDUCTION)
ı								
	117	191	8e-23	-0.46	0.00		QGSR ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX	COMPLEX (ZINC FINGER/DNA),

PDB annotation	ZINC FINGER, DNA-BINDING PROTEIN	COMPLEX (ZINC FINGER/DNA)	COMPLEX (ZINC FINGER/DNA),	PROTEIN	COMPLEX (ZINC FINGER/DNA)	COMPLEX (ZINC FINGER/DNA),	ZINC FINGER, DNA-BINDING	COMPLEX (ZINC FINGER/DNA)	COMPLEX (ZINC FINGER/DNA),	ZINC FINGER, DNA-BINDING	PROTEIN	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA),	ZINC FINGER, DNA-BINDING	PROTEIN	COMPLEX (ZINC FINGER/DNA)	COMPLEX (ZINC FINGER/DNA),	PROTEIN	┢		•						COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA	INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRICTINE COMPLEX
Coumpound	OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	QGSR ZINC FINGER PEPTIDE;	CHAIN: A; DUPLEX OF IGONFICE BOTTOF RINDING	SITE; CHAIN: B, C;	QGSR ZINC FINGER PEPTIDE;	CHAIN: A; DUPLEX	OLIGONUCLEOTIDE BINDING SITE: CHAIN: B. C.	OGSR ZINC FINGER PEPTIDE;	CHAIN: A; DUPLEX	OLIGONUCLEOTIDE BINDING	SILE; CHAIN: B, C;	QGSR ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX	OLIGONUCLEOTIDE BINDING	SITE; CHAIN: B, C;	QGSR ZINC FINGER PEPTIDE;	CHAIN: A; DUPLEX Or 1900/11/01 EOTHDE BENTALIO	SITE; CHAIN: B, C;	TRANSCRIPTION REGULATION	YEAST TRANSCRIPTION	FACTOR ADRI (RESIDUES 102 -	130) 1ARD 3 (AMINO	TERMINAL ZINC FINGER	DOMAIN) (NIMR, 10	STRUCTURES) 1ARD 4 (ADR1B)	JARD 5	DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER	PROTEIN; CHAIN: C, F, G;
SEQFOL D score		75.37					-																				
PMF score			_		6.93			0.25				0.33			0.87			0.81								0.22	
Verify score					-0.18			90.0				-0.34			-0.66			-0.12							,	-0.12	
Psi Blast		6.4e-30			6.4e-30	· 		3.2e-26				6.4e-24			6.4e-30			1.6e-06								1.6e-38	
END		249			247	•		281				400			428		,	376								191	
STAR T AA		166			167			195				325			348			348								109	
CEAI N ID		¥			Ą			A				⋖			٠ ٧	•				_						ပ	
PDB ID		lalh			laih	***************************************		laih		tivino		la h			laih			lard						-		Imey	
SEQ ID NO:		1841			1841			1841				1841	•		1841	,		1841								1841	

Imey C 138 219 1.6e-47 -0.01 0.98 DNA; CHADN: A, B, D, E; CONSENSUS ZNC FROGER PROTEIN; CHAIN: C, F, G; CHADN:	Se US	PDB	CHAI	STAR T AA	END	Psi Blast	Verify	PMF score	SEQFOL D score	Coumpound	PDB annotation
C 138 219 1.6e-47 -0.01 0.98 DNA; CHANN: A, B, D, E; CONSENSUS ZING FINGER PROTEIN; CHAIN: G, F, G; CONSENSUS ZING FINGER PROTEIN; CHAIN: A, B, D, E; CONSENSUS ZING FINGER PROTEIN; CHAIN: A, B, D, E; CONSENSUS ZING FINGER PROTEIN; CHAIN: C, F, G; CONSENSUS ZINGER PROTEIN; CHAIN											(ZINC FINGER/DNA)
Imey C 166 247 1.66-48 0.11 1.00 DNA; CHAIN; C, F, G;	1841	Imey	ပ	138	219	1.6e-47	-0.01	0.98		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA
Imey C 166 247 1.66-48 0.11 1.00 DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G; 1.66-48 1.66-48 1.66-48 1.66-48 1.66-48 1.66-45 1.66-45 1.66-45 1.66-45 1.66-45 1.66-45 1.66-45 1.66-45 1.66-45 1.66-45 1.66-45 1.66-45 1.66-45 1.66-45 1.66-45 1.66-45 1.66-45 1.66-45 1.66-45 1.66-45 1.66-45 1.66-45 1.66-45 1.66-45 1.66-45 1.66-45 1.66-45 1.66-45 1.66-45 1.66-45 1.66-45 1.66-45 1.66-45 1.66-45 1.66-45 1.66-45 1.66-45 1.66-45 1.66-45 1.66-45 1.66-45 1.66-45 1.66-45 1.66-45 1.66-45 1.66-45 1.66-45 1.66-45 1.66-45 1.66-45 1.66-45 1.66-45 1.66-45 1.66-45 1.66-45 1.66-45 1.66-45 1.66-45 1.66-45 1.66-45 1.66-45 1.66-45 1.66-45 1.66-45 1.66-45 1.66-45 1.66-45 1.66-45 1.66-45 1.66-45 1.66-45 1.66-45 1.66-45 1.66-45 1.66-45 1.66-45 1.66-45 1.66-45 1.66-45 1.66-45 1.66-45 1.66-45 1.66-45 1.66-45 1.66-45 1.66-45 1.66-45 1.66-45 1.66-45 1.66-45 1.66-45 1.66-45 1.66-45 1.66-45 1.66-45 1.66-45 1.66-45 1.66-45 1.66-45 1.66-45 1.66-45 1.66-45 1.66-45 1.66-45 1.66-45 1.66-45 1.66-45 1.66-45 1.66-45 1.66-45 1.66-45 1.66-45 1.66-45 1.66-45 1.66-45 1.66-45 1.66-45 1.66-45 1.66-45 1.66-45 1.66-45 1.66-45 1.66-45 1.66-45 1.66-45 1.66-45 1.66-45 1.66-45 1.66-45 1.66-45 1.66-45 1.66-45 1.66-45 1.66-45 1.66-45 1.66-45 1.66-45 1.66-45 1.66-45 1.66-45 1.66-45 1.66-45 1.66-45 1.66-45 1.66-45 1.66-45 1.66-45 1.66-45 1.66-45 1.66-45 1.66-45 1.66-45 1.66-45 1.66-45 1.66-45 1.66-45 1.66-45 1.66-45 1.66-45 1.66-45 1.66-45 1.66-45 1.66-45 1.66-45 1.66-45 1.66-45 1.66-45 1.66-45 1.66-45 1.66-45 1.66-45 1.66-45 1.66-45 1.66-45 1.66-45 1.66-45 1.66-45 1.66-45 1.66-45 1.66-45 1.66-45 1.66-45 1.66-45 1.66-45 1.66-45 1.66-45 1.66-45 1.66-4										PROTEIN; CHAIN: C, F, G;	INTERACTION, PROTEIN DESIGN, 2
Imey C 166 247 1.66-48 0.11 1.00 DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G; 1.66-48 1.66-48 1.66-48 1.66-45 -0.14 0.22 DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G; 1.66-45 -0.14 0.22 DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G; 1.66-45 -0.19 0.82 DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G; 1.66-45 -0.19 0.82 DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G; 1.66-45 -0.19 0.82 DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G; 1.66-45 -0.19 0.82 DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G; CONSENSUS ZINC FINGER PROTEIN; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G; CONSENSUS ZINC FINGER PROTEIN; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G; CONSENSUS ZINC FINGER PROTEIN; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G; CONSENSUS ZINC FINGER PROTEIN; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G; C,											CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
Imey C 166 248 1.6e-48 83.84 DNA; CHAIN: C, F, G; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G; C, CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G; C, CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G; C, C, CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G; C,		1mey	J	166	247	1.6e-48	0.11	1.00		DNA; CHAIN: A, B, D, E;	COMPLEX (ZINC FINGED DNA) ZINC
Imey C 166 248 1.66-48 83.84 DNA; CHAIN; C, F, G;	-		,	V						CONSENSUS ZINC FINGER	FINGER, PROTEIN-DNA
Imey C 166 248 1.6e-48 83.84 DNA; CHAIN: A, B, D, E; Imey C 194 282 8e-45 -0.14 0.22 DNA; CHAIN: C, F, G; Imey C 194 282 8e-45 -0.14 0.22 DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G; CONSENSUS ZINC FINGER Imey C 324 400 1.1e-41 -0.60 0.22 DNA; CHAIN: A, B, D, E; Imey C 347 428 1.6e-45 -0.19 0.82 DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G; Imey G 220 247 1.1e-12 0.13 0.70 DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;			•							PROTEIN; CHAIN: C, F, G;	INTERACTION, PROTEIN DESIGN, 2
Imey C 166 248 1.6e-48 83.84 DNA; CHAIN: A, B, D, E, CONSENSUS ZINC FINGER Imey C 194 282 8e-45 -0.14 0.22 DNA; CHAIN: A, B, D, E, CONSENSUS ZINC FINGER Imey C 324 400 1.1e-41 -0.60 0.22 DNA; CHAIN: A, B, D, E, CONSENSUS ZINC FINGER Imey C 347 428 1.6e-45 -0.19 0.82 DNA; CHAIN: A, B, D, E, CONSENSUS ZINC FINGER Imey C 347 428 1.6e-45 -0.19 0.82 DNA; CHAIN: A, B, D, E, CONSENSUS ZINC FINGER Imey G 320 247 1.1e-12 0.13 0.70 DNA; CHAIN: A, B, D, E, CONSENSUS ZINC FINGER				,,							CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
Imey C 194 282 86-45 -0.14 0.22 DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G; CONSENSUS ZINC FINGER PROTEIN; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G; CONSENSUS ZINC FINGER PROTEIN; C, F, G, C, C, CONSENSUS ZINC FINGER PROTEIN; C, F, G, C, C, CONSENSUS ZINC FINGER PROTEIN; C, F, G, C,	L	Imey	C	166	248	1.6e-48			83.84	DNA; CHAIN: A, B, D, E;	COMPLEX (ZINC FINGER/DNA) ZINC
Imey C 194 282 86-45 -0.14 0.22 DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G; CONSENSUS ZINC FINGER PROTEIN; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G; C, CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G; C, CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G; C, CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G; C, CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G; C, CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G; C, CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G; C, CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G; C, CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G; C, CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G; C, CONSENSUS ZINC FINGER PROTEIN; C, C, C, C, CONSENSUS ZINC FINGER PROTEIN; C, C, C, C, CONSENSUS ZINC FINGER PROTEIN; C,		•		~~~		-				CONSENSUS ZINC FINGER	FINGER, PROTEIN-DNA
Imey C 194 282 86-45 -0.14 0.22 DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G; Imey C 324 400 1.16-41 -0.60 0.22 DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER Imey C 347 428 1.66-45 -0.19 0.82 DNA; CHAIN: A, B, D, E; Imey C 347 428 1.66-45 -0.19 0.82 DNA; CHAIN: A, B, D, E; Imey G 220 247 1.16-12 0.13 0.70 DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN: CHAIN: C, F, G; CONSENSUS ZINC FINGER PROTEIN: CHAIN: C, F, G;										PROTEIN; CHAIN: C, F, G;	INTERACTION, PROTEIN DESIGN, 2
Imey C 194 282 8e-45 -0.14 0.22 DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G; Imey C 324 400 1.1e-41 -0.60 0.22 DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G; Imey C 347 428 1.6e-45 -0.19 0.82 DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G; Imey G 220 247 1.1e-12 0.13 0.70 DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G; C,						,					CRYSTAL STRUCTURE, COMPLEX
C 194 282 8e-45 -0.14 0.22 DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G; C 324 400 1.1e-41 -0.60 0.22 DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G; C 347 428 1.6e-45 -0.19 0.82 DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G; C 220 247 1.1e-12 0.13 0.70 DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN: CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN: CHAIN: C, F, G; C CONSENSUS ZINC FINGER PROTEIN: CHAIN: C, F, G; C CONSENSUS ZINC FINGER PROTEIN: CHAIN: C, F, G; C CONSENSUS ZINC FINGER PROTEIN: CHAIN: C, F, G; C CONSENSUS ZINC FINGER PROTEIN: CHAIN: C, F, G; C CONSENSUS ZINC FINGER PROTEIN: CHAIN: C, F, G; C CONSENSUS ZINC FINGER PROTEIN: C, F, G; C C, C											(ZINC FINGER/DNA)
Imey C 324 400 1.1e-41 -0.60 0.22 DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G; Imey C 347 428 1.6e-45 -0.19 0.82 DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G; Imey G 220 247 1.1e-12 0.13 0.70 DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	_	Imey	ပ	194	282	8e-45	-0.14	0.22		DNA; CHAIN: A, B, D, E;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER PROTEIN-DNA
Imey C 324 400 1.1e-41 -0.60 0.22 DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G; Imey C 347 428 1.6e-45 -0.19 0.82 DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G; CONSENSUS ZINC FINGER CONSENSUS ZINC FINGER CONSENSUS ZINC FINGER PROTEIN; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN: CHAIN: C, F, G; CONSENSUS ZINC FINGER PROTEIN: CHAIN: C, F, G; CONSENSUS ZINC FINGER PROTEIN: CHAIN: C, F, G; CONSENSUS ZINC FINGER PROTEIN: C, F, G; C,										PROTEIN: CHAIN: C. F. G:	INTERACTION, PROTEIN DESIGN, 2
Imey C 324 400 1.1e-41 -0.60 0.22 DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G; Imey C 347 428 1.6e-45 -0.19 0.82 DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G; CONSENSUS ZINC FINGER CONSENSUS ZINC FINGER CONSENSUS ZINC FINGER PROTEIN; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN: CHAIN: C, F, G; CONSENSUS ZINC FINGER PROTEIN: C, F, G; C,											CRYSTAL STRUCTURE, COMPLEX
Imey C 324 400 1.1e-41 -0.60 0.22 DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G; C 347 428 1.6e-45 -0.19 0.82 DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G; Imey G 220 247 1.1e-12 0.13 0.70 DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN: CHAIN: C, F, G; CONSENSUS ZINC FINGER PROTEIN: CHAIN: C, F, G; CONSENSUS ZINC FINGER PROTEIN: CHAIN: C, F, G; C CONSENSUS ZINC FINGER PROTEIN: CHAIN: C, F, G; C C C C C C C C C	-										(ZINC FINGER/DNA)
Imey C 347 428 1.6e-45 -0.19 0.82 DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G; Imey G 220 247 1.1e-12 0.13 0.70 DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G; CONSENSUS ZINC FINGER PROTEIN: CHAIN: C, F, G; C,	_	lmey	ပ	324	400	1.1e-41	-0.60	0.22		DNA; CHAIN: A, B, D, E;	COMPLEX (ZINC FINGER/DNA) ZINC
Imey C 347 428 1.6e-45 -0.19 0.82 DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G; Imey G 220 247 1.1e-12 0.13 0.70 DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN: CHAIN: C, F, G; CONSENSUS ZINC FINGER										CONSENSUS ZINC FINGER	FINGER, PROTEIN-DNA
Imey C 347 428 1.6e-45 -0.19 0.82 DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G; Emery Imey G 220 247 1.1e-12 0.13 0.70 DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN: CHAIN: C F G.										PROTEIN; CHAIN: C, F, G;	INTERACTION, PROTEIN DESIGN, 2
Imey C 347 428 1.6e-45 -0.19 0.82 DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G; Imey G 220 247 1.1e-12 0.13 0.70 DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN: CHAIN: C, F, G; CONSENSUS ZINC FINGER											CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;		Imey	ပ	347	428	1.6e-45	-0.19	0.82		DNA; CHAIN: A, B, D, E;	COMPLEX (ZINC FINGER/DNA) ZINC
PROTEIN; CHAIN: C, F, G;										CONSENSUS ZINC FINGER	FINGER, PROTEIN-DNA
Imey G 220 247 I.1e-12 0.13 0.70 DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER										PROTEIN; CHAIN: C, F, G;	INTERACTION, PROTEIN DESIGN, 2
Imey G 220 247 1.1e-12 0.13 0.70 DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER											CRYSTAL STRUCTURE, COMPLEX
1mey G 220 247 1.1e-12 0.13 0.70 DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN: CHAIN: C. F. G.											(ZINC FINGER/DNA)
	-	1mey	9	220	247	1.le-12	0.13	0.70		DNA; CHAIN: A, B, D, E;	COMPLEX (ZINC FINGER/DNA) ZINC
_										PROTEIN: CHAIN: C. F. C.	FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2

PDB guacaien	CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA	INTERACTION, PROTEIN DESIGN, 2	CRYSTAL STRUCTURE, COMPLEX	(ZINC FINGER/DNA)	COMPLEX (ZINC FINGER/DNA) ZINC	FINGER, PROTEIN-DINA INTERACTION PROTEIN DESIGN 2	CRYSTAL STRUCTURE, COMPLEX	(ZINC FINGER/DNA)	ZINC FINGER TRANSCRIPTION	FACTOR SP1; ZINC FINGER,	TRANSCRIPTION ACTIVATION, SP1	COMPLEX (TRANSCRIPTION	REGULATION/DNA) TFIIIA; 58	GENE; NMR, TFIIIA, PROTEIN, DNA.	TRANSCRIPTION FACTOR, 5S RNA 2	GENE, DNA BINDING PROTEIN,	ZINC FINGER, COMPLEX 3	(TRANSCRIPTION	REGULATION/DNA)	COMPLEX (TRANSCRIPTION	REGULATION/DNA) COMPLEX	(TRANSCRIPTION	REGULATION/DNA), RNA	POLYMERASE III, 2	TRANSCRIPTION INITIATION, ZINC	FINGER PROTEIN	COMPLEX (TRANSCRIPTION	(TRANSCRIPTION	REGULATION/DNA), RNA
Coumpound		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER	PROTEIN; CHAIN: C, F, G;		ב מינייים אומי	DNA; CHAIN: A, B, D, E;	PROTEIN CHAIN OF G			SPIF2; CHAIN: NULL;			TRANSCRIPTION FACTOR IIIA;	CHAIN: A; 5S RNA GENE;	CHAIN: E, F;						TFIIIA; CHAIN: A, D; 5S	RIBOSOMAL RNA GENE,	CHAIN: B, C, E, F;					TFIIIA; CHAIN: A, D; 5S	CHAIN: B C E F.	
SEQFOL D score								,													74.20		4	•	4					
PMF		0.95			07.0	0,48				0.03			-0.11						_									0.49		
Verify score		-0.26			60.0	0.03		·		-0.21			0.03												_			-0.25		
Psi Blast		6.4e-13			1 62 12	1.06-13				8e-00			1.1e-20								3.2e-33							3.2e-33		
END		372			400	674				376			267								278							284		
STAR T AA		345			401	104				348			195			_					112							139		
CHAI N ID		ຍ			C								∀								∢							₹		
PDB ID		Imey			1	imey		_		lsp2			<u> </u>								1116							1£6		
SEQ ID NO:		1841			1041	1401				1841			1841								1841							1841		

Verify PMF score
-0.30 0.19
7
-0.37 0.04
-0.16 0.19
77.97
vil Rivata - 4
020
1

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PDB annotation	REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2	FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION.	INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGIL ATTOMONA)	COMPLEX (TRANSCRIPTION REGULATIONDNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX	REGULATION/DNA)			COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI;	GLI, ZINC FINGER, COMPLEX (DNA- BINDING PROTEIN/DNA)	COMPLEX (DNA-BINDING
Coumpound	ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;		YYI; CHAIN: C; ADENO- ASSOCIATED VIRUS P5 INITIATOR ELEMENT DINA;	CHAIN: A, B;	YYI; CHAIN: C; ADENO- ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX(TRANSCRIPTION	REGULATION/DNA) TRAMTRACK PROTEIN (TWO ZINC-FINGER PEPTIDE)	COMPLEXED WITH 2DRP 3 DNA 2DRP 4	ZINC FINGER PROTEIN GLII; CHAIN: A; DNA; CHAIN: C, D;		ZINC FINGER PROTEIN GLII;
SEQFOL D score									76.50		
PNTF score			0,04		0.40	0.01					0.62
Verify score			-0.25		-0.46	-0.52					-0.12
Psi Blast		,	3.2e-32		6.4e-30	4.8e-06			I.6e-32		6e-29
END AA			281		428	371			783		252
STAR T AA	•		174		332	323			138		140
CHAI N ID			ပ		v	A			•		A
PDB ID			lubd		P p q n	2drp					2gli
SEQ ID NO:			1841		80 14	1841			1841		1841

	-k	A-	Γ				T	16.					.,,				_					٠,	 ;<			
PDB annotation	PROTEINDNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA- BINDING PROTEINDNA)	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA- BINDING PROTEIN/DNA)		STRUCTURAL PROTEIN TWO	REPEATS OF SPECTRIN, ALPHA HELICAL LINKER REGION 22	TANDEM 3-HELIX COLLED-COLLS,	STRICTIBAL PROTEIN	REPEATS OF SPECTRIN ALPHA	HELICAL LINKER REGION, 22	TANDEM 3-HELIX COILED-COILS,	SIRUCTURAL PROTEIN	ENDOCYTOSIS/EXOCYTOSIS	NSEC1; PROTEIN-PROTEIN	COMPLEX, MULTI-SUBUNIT	ENDOCYTOSIS/EXOCYTOSIS	NSEC1; PROTEIN-PROTEIN	COMPLEX, MULTI-SUBUNIT	ENDOCYTOSIS/EXOCYTOSIS	NSECI; PROTEIN-PROTEIN	COMPLEX, MULTI-SUBUNIT	ENDOCYTOSIS/EXOCYTOSIS	SYNAPTOTAGMIN ASSOCIATED 35	KDA PROTEIN, P35A, THREE HELIX	BUNDLE	ENDOCYTOSIS/EXOCYTOSIS	SYNAPTOTAGMIN ASSOCIATED 35
Coumpound	CHAIN: A; DNA; CHAIN: C, D;	ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;		IA SPECTRIN; CHAIN: A,	S n		AI PHA SPECTRIN: CHAIN: A					Z	A; SYNTAXIN 1A;	Ŧ	Z	A; SYNTAXIN IA;	+	_ Z	A; SYNTAXIN IA;	-	SYNTAXIN-1A; CHAIN: A, B, C; E	~ 1			SYNTAXIN-1A; CHAIN: A, B, C; E	
SEQFOL D score	·																									
PMF score		-0.05		-0.17			0.00					-0.20			-0.20		i,	-0.17		9	 6.19				-0.19	
Verify score		0.09		1.09			0.39				,	0.41			0.57		,,,	U.43		9	 6.78				0.83	
Psi Blast		1.6e-32		I.5e-09			7.5e-05				\dagger	4.3e-10		\dagger	1.5e-17		1	1.50.1	····	T	6-0A			1	3e-10	
END		283		848			798];	513			242		260	5		Ť	0/0				100	
STAR		146		511			566				114	754		.07	481		513	J.		147	Ì			200		-
CHAI N ID		¥		¥	1		A			•	٦	a		¢	מ		_	-		_	ς .				ς.	
PDB		2gli		ncm 1			1cun				1,42.1			177	Tun		idn1	1	•	1072	3			5	152	
SEQ NO:		1841	;	1845			1845				1015	1040		1045	1040	-	1845	2		1845	C+o-		_	1015	1040	_

	PDB annotation	BUNDLE	ENDOCYTOSIS/EXOCYTOSIS SYNAPTOTAGMIN ASSOCIATED 35 KDA PROTEIN, P35A, THREE HELLX BUNDLE	ENDOCYTOSIS/EXOCYTOSIS SYNAPTOTAGMIN ASSOCIATED 35 KDA PROTEIN, POWESFIKEE HELIX BUNDLE	ENDOCYTOSIS/EXOCYTOSIS SYNAPTOTAGMIN ASSOCIA TED 35 KDA PROTEIN, P35A, THREE HELIX BUNDLE	SIGNALING PROTEIN GBP, GTP HYDROLYSIS, GDP, GWP, INTERFERON INDUCED, DYNAMIN 2 RELATED, LARGE GTPASE FAMILY, GMPPNP, GPPNHP.	MEMBRANE PROTEIN FOUR HELIX BUNDLE, ALPHA HELIX	CONTRACTILE PROTEIN TRIPLE- HELIX COILED COIL, CONTRACTILE PROTEIN	ISOMERASE ISOMERASE, MUTASE, INTRAMOLECULAR TRANSFERASE	TRANSCRIPTION REGULATION SIGMA70; RNA POLYMERASE SIGMA FACTOR, TRANSCRIPTION REGIL ATION	TRANSCRIPTION REGULATION SIGMA70; RNA POLYMERASE SIGMA FACTOR, TRANSCRIPTION REGILLATION	COMPLEX
	Coumpound		SYNTAXIN-1A; CHAIN: A, B, C;	SYNTAXIN-1A; CHAIN: A, B, C;	SYNTAXIN-1A; CHAIN: A, B, C;	INTERFERON-INDUCED GUANYLATE-BINDING PROTEIN 1; CHAIN: A;	SSOI PROTEIN; CHAIN: A;	HUMAN SKELETAL MUSCLE ALPHA-ACTININ 2; CHAIN: A;	METHYLMALONYL-COA MUTASE: CHAIN: A. B. C. D:	RNA POLYMERASE PRIMARY SIGMA FACTOR; CHAIN: NULL;	RNA POLYMERASE PRIMARY SIGMA FACTOR; CHAIN: NULL;	TRANSDUCIN; CHAIN: B, G;
n Northern of Art Griffelier (Die Bei Geogriffeliere (Arton	SEQFOL D score											
	PMF score		-0.20	-0.17	0.00	-0.19	-0.20	-0.19	-0.08	-0.15	-0.20	-0.20
granik izeneile.	Verify score		1.11	96.0	0.21	0.74	0.55	0.70	0.48	0.76	0.40	0.22
	Psi Blast		1.56-16	3e-16	4.5e-05	3e-08	9e-13	3e-24	4.5e-31	4.5e-18	6e-17	1.5e-17
	END AA		0630	859	198	626	642	656	746	643	677	621
	STAR T AA		511	526	739	485	485	460	451	485	486	488
	CHAI N ID		∢	¥	• ¥	¥	A	∢	₩.			Ъ
	PDB ID		1ez3	lez3] ez3	lf5n	1fio		Ireq	lsig	1sig	2trc
	SEQ ID NO:		1845	1845	1845	1845	1845	1845	1845	1845	1845	1845

PDB annotation	(TRANSDUCER/TRANSDUCTION) GT BETA-GAMMA; MEKA, PP33; PHOSDUCIN, TRANSDUCIN, BETA-GAMMA, SIGNAL TRANSDUCTION,	2 KEGULATION, PHOSPHORYLATION, G PROTEINS, THIOREDOXIN, 3 VISION, MEKA, COMPLEX (TRANSDUCER/TRANSDUCTION)	COMPLEX (TRANSDUCER/TRANSDUCTION) GT BETA-GAMMA; MEKA, PP33; PHOSDUCIN, TRANSDUCIN, BETA-	GAMMA, SIGNAL TRANSDUCTION, 2 REGULATION, PHOSPHORYLATION, G PROTEINS, THIOREDOXIN, 3 VISION. MEKA.	COMPLEX (TRANSDUCER/TRANSDUCTION)	COMPLEX (TRANSDUCER/TRANSDUCTION) GT BETA-GAMMA: MEKA, PP33:	PHOSDUCIN, TRANSDUCIN, BETA-GAMMA, SIGNAL TRANSDUCTION,	PHOSPHORYLATION, G PROTEINS, THIOREDOXIN, 3 VISION, MEKA,	COMPLEX (TRANSDUCER/TRANSDUCTION)	TRANSCRIPTION REGULATION PROTO-ONCOGENE, NUCLEAR BODIES (PODS), LEUKEMIA, 2 TRANSCRIPTION REGULATION
Coumpound	PHOSDUCIN; CHAIN: P;		TRANSDUCIN; CHAIN: B, G; PHOSDUCIN; CHAIN: P;			TRANSDUCIN; CHAIN: B, G; PHOSDUCIN; CHAIN: P;				TRANSCRIPTION FACTOR PML; CHAIN: NULL;
SEQFOL D score										
PMF			-0.19			-0.20				0.59
Verify			0.29			0.23				-0.68
Psi Blast			1.5e-20	10		1.5e-13			-	1.1e-07
END			647			746				55
STAR T AA			513			577				59
CHAI N ID	4		р.			A.				
PDB ID			2thc	· · · · · · · · · · · · · · · · · · ·		2trc				1 bor
SEQ ID NO:			1845			1845				1849

PDB annotation	ACTIN BINDING PROTEIN ABP-120; ACTIN BINDING PROTEIN, STRUCTURE, IMMUNOGLOBULIN, GELATION 2 FACTOR APP-120	ACTIN BINDING PROTEIN ABP-120; ACTIN BINDING PROTEIN, STRUCTURE, IMMUNOGLOBULIN, GELATION 2 FACTOR APP-120	ACTIN BINDING PROTEIN ABP-120; ACTIN BINDING PROTEIN, STRUCTURE, IMMUNOGLOBULIN, GEI ATION 2 FACTOR APP-120	ACTIN BINDING PROTEIN ACTIN BINDING PROTEIN, 120; ACTIN BINDING PROTEIN, IMMUNOGLOBULIN, GELATION FACTOR, ARP. 2 120	ACTION BINDING PROTEIN ACTIN BINDING PROTEIN 120; ACTIN BINDING PROTEIN, IMMUNOGLOBULIN, GELATION FACTOR, ABP. 2, 120	ACTIN BINDING PROTEIN ACTIN BINDING PROTEIN 120; ACTIN BINDING PROTEIN, IMMUNOGLOBULIN, GELATION FACTOR, ARP. 2 120	ACTIN BINDING PROTEIN ACTIN BINDING PROTEIN 120; ACTIN BINDING PROTEIN, IMMUNOGLOBULIN, GELATION FACTOR, ABP-2 120	TRANSFERASE
Coumpound	GELATION FACTOR; CHAIN: NULL;	GELATION FACTOR; CHAIN: NULL;	GELATION FACTOR; CHAIN: NULL;	GELATION FACTOR; CHAIN: A, B;	GELATION FACTOR; CHAIN: A, B;	GELATION FACTOR; CHAIN: A, B;	GELATION FACTOR; CHAIN: A, B;	GLYCINE N-
SEQFOL D score	64.85			62.06				
PMF score	·	0.99	1.00	•	0.95	96.0	0.99	0.21
Verify		0.47	0.54		0.11	0.52	0.52	-0.00
Psi Blast	4.5e-30	4.5e-30	1.3e-19	6e-36	1.6e-13	1.3e-19	6e-3 <i>6</i>	7.še-06
END	200	498	499	515	494	528	528	331
STAR T AA	397	398	398	306	359	395	397	175
CHAI N ID	7. 100			٧	¥	4	4	A
PDB ID	1ksr	1ksr	1ksr	1qfh			14th	1d2h
SEQ ON ON	1849	1849	1849	1849	1849	1849	1849	1850

PDB annotation	METHYLTRANSFERASE	STRUCTURAL GENOMICS HYPOTHETICAL PROTEIN, METHANOCOCCIS JANNA SCHII	TRANSFERASE SAM-BINDING	DOMAIN, BETA-BARREL, MIXED	ALPHA-BETA, HEXAMER, 2 DIMER		ANTI-ONCOGENE CELL CYCLE, ANTI-ONCOGENE, REPEAT, ANK REPEAT											A ANI PY (TE ANIOCEPATION)	COWILTEA (TRANSCRIPTION	KEGULATION/DNA) GABPALPHA;	GABPBETA1; COMPLEX	TRANSCRIPTION	REGULATION/DNA), DNA-BINDING,	2 NUCLEAR PROTEIN, ETS DOMAIN.	ANKYRIN REPEATS,	TRANSCRIPTION 2 FACTOR	COMPLEX (TRANSCRIPTION	REGULATION/DNA) GABPALPHA;	GABPBETA1; COMPLEX
Coumpound	METHYLTRANSFERASE; CHAIN: A, B, C, D;			ASE;	CHAIN: 1, 2, 3, 4, 5, 6;		TUMOR SUPPRESSOR P16INK4A; CHAIN: NULL;	HOTRA	NSFERASE) \$C-/AMP\$-	DEPENDENT PROTEIN KINASE	(E.C.2.7.1.37) (\$C/APK\$) 1APM 3	(CATALYTIC SUBUNIT) ALPHA	ISOENZYME MUTANT WITH	SER 139 1APM 4 REPLACED BY	ALA (/S139A\$) COMPLEX WITH	THE PEPTIDE 1APM 5	INHIBITOR PKI(5-24) AND THE	CA PINION PROTENT AT 1114			CHAIN: B;	DNA; CHAIN: D, E;					ALPHA;		PROTEIN BETA 1; CHAIN: B; (
SEQFOL D score								99.80							-						 								
PMF		0.01	0.04				0.95											1 00	200								00: <u>1</u>		
Verify score	-	0.24	0.11				0.39										_	A 33)								0.55		
Psi Blast		6.4e-09	1.3e-14				4.5e-32	4.5e-30			Addient							1.5e-36)							1	7.5e-43		_
END AA		294	292			,	668	349										604							***		637		
STAR T AA		177	148				538			_								447									486		
CHAI N ID		₹ .	_					ш									*****	В					-					•	
PDB ID		1dus	1g6q				lase	lapm		-							-	lawc	-							╅	Tawc		
SEQ ID NO:		1850	1850			5.5	1833	1853					•					1853	-							0101	1833		

PDB CHAI STAR END Psi Blast Verify D NID TAA AA score	STAR END Psi Blast TAA AA	END Psi Blast AA	Psi Blast	ast	Verify		PMF score	SEQFOL D score	Coumpound	PDB annotation
						The second liverage and the se			DNA; CHAIN: D, E;	(TRANSCRIPTION REGULATION/DNA), DNA-BINDING, 2 NUCLEAR PROTEIN, ETS DOMAIN, ANKYRIN REPEATS, TRANSCRIPTION 3 FACTOR
lawc B 551 705 1.2e-45	551 705	705	<u>- </u>	1.2e-45				94.92	GA BINDING PROTEIN ALPHA; CHAIN: A; GA BINDING PROTEIN BETA I; CHAIN: B; DNA; CHAIN: D, E;	COMPLEX (TRANSCRIPTION REGULATION/DNA) GABPALPHA; GABPBETAI; COMPLEX (TRANSCRIPTION REGULATION/DNA), DNA-BINDING, 2 NUCLEAR PROTEIN, ETS DOMAIN, ANKYRIN REPEATS, TRANSCRIPTION 3 PACTOR
lawc B 556 704 6.4e-35 0.72	556 704 6.4e-35	704 6.4e-35	6.46-35		0.72		1.00		GA BINDING PROTEIN ALPHA; CHAIN: A; GA BINDING PROTEIN BETA 1; CHAIN: B; DNA; CHAIN: D, E;	COMPLEX (TRANSCRIPTION REGULATION/DNA) GABPALPHA; GABPBETAI; COMPLEX (TRANSCRIPTION REGULATION/DNA), DNA-BINDING, 2 NUCLEAR PROTEIN, ETS DOMAIN, ANK YRIN REPEATS, TRANSCRIPTION? FACTOR
	• 584 737 1.2e-45	737 1.2e-45	1.2e-45		0.70		1.00		GA BINDING PROTEIN ALPHA; CHAIN: A; GA BINDING PROTEIN BETA 1; CHAIN: B; DNA; CHAIN: D, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) GABPALPHA; GABPBETA!; COMPLEX (TRANSCRIPTION REGULATION/DNA, DNA-BINDING, 2 NUCLEAR PROTEIN, ETS DOMAIN, ANKYRIN REPEATS, TRANSCRIPTION 3 FACTOR
lawc B 617 770 1.5e-44 0.60	617 770 1.5e-44	770 1.5e-44	1.5e-44		09.0		1.00		GA BINDING PROTEIN ALPHA; CHAIN: A; GA BINDING PROTEIN BETA 1; CHAIN: B; DNA; CHAIN: D, E;	COMPLEX (TRANSCRIPTION REGULATION/DNA) GABPALPHA; GABPBETA1; COMPLEX (TRANSCRIPTION/ REGULATION/DNA), DNA-BINDING,

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PDB annotation	2 NUCLEAR PROTEIN, ETS DOMAIN, ANKYRIN REPEATS, TRANSCRIPTION 3 FACTOR	COMPLEX (TRANSCRIPTION REGULATION/DNA) GABPALPHA; GABPBETA1; COMPLEX (TRANSCRIPTION	REGULATION/DNA), DNA-BINDING, 2 NUCLEAR PROTEIN, ETS DOMAIN, ANKYRIN REPEATS, TRANSCRIPTIONS TRANSTR	COMPLEX (TRANSCRIPTION REGULATION/DNA) GABPALPHA;	GABPBETA1; COMPLEX (TRANSCRIPTION	REGULATION/DNA), DNA-BINDING, 2 NUCLEAR PROTEIN, ETS DOMAIN,	ANKYRIN REPEATS, TRANSCRIPTION 3 FACTOR	COMPLEX (TRANSCRIPTION REGIL ATTONONA) GARPALPHA:	GABPBETA1; COMPLEX	(TRANSCRIPTION REGULATION/DNA), DNA-BINDING	2 NUCLEAR PROTEIN, ETS DOMAIN,	ANKYRIN REPEATS, TRANSCRIPTION 3 FACTOR	COMPLEX (ISOMERASE/PROTEIN KINASE) FKBP12:	SERINE/THREONINE-PROTEIN	KINASE KECEF I OK R4; COMPLEX (ISOMERA SE/PROTEIN KINASE)	RECEPTOR 2 SERINE/THREONINE KINASE
Coumpound		GA BINDING PROTEIN ALPHA; CHAIN: A; GA BINDING PROTEIN BETA I; CHAIN: B; DNA; CHAIN: D, E;		GA BINDING PROTEIN ALPHA; CHAIN: A; GA BINDING	PROTEIN BETA I; CHAIN: B; DNA; CHAIN: D, E;			GA BINDING PROTEIN ALPHA; CHAIN: A: GA BINDING	PROTEIN BETA 1; CHAIN: B;	DNA; CHAIN: D, E;			FK506-BINDING PROTEIN; CHAIN: A. C. E. G. TGF-B	SUPERFAMILY RECEPTOR	IYPE I; CHAIN: B, D, F, H;	
SEQFOL D score			-	* .										-		
PIMF score	·	1.00		1.00				1.00					1.00			
Verify score	1.	0.63		0.34				0.74					0.37			
Psi Blast	·	1.5e-42	-	1.6e-32				3e-35					3e-49			
END		. 802		802	. 17780	ones.		828					376			
STAR T AA		651		656				687					26			
CHAI N ID		В		a				В	-				В			
202 CI		lawc		lawc			;	lawc			-		1 b 6c			
SEQ ID NO:		1853		1853				1853					1853			

			,						
PDB annotation	TUMOR SUPPRESSOR TUMOR SUPPRESSOR, CDK4/K DILIBITOR, ANKYRIN MOTIF	TUMOR SUPPRESSOR TUMOR SUPPRESSOR, CDK4/6 INHIBITOR, ANKYRIN MOTIF	TUMOR SUPPRESSOR TUMOR SUPPRESSOR, CDK4/6 INHIBITOR, ANKYRIN MOTIF	COMPLEX (INHIBITOR PROTEIN/KINASE) INHIBITOR PROTEIN, CYCLIN-DEPENDENT KINASE, CELL CYCLE 2 CONTROL, ALPHA/BETA, COMPLEX (INHIBITOR PROTEIN/KINASE)	COMPLEX (INHIBITOR PROTEIN/KINASE) INHIBITOR PROTEIN, CYCLIN-DEPENDENT KINASE, CELL CYCLE 2 CONTROL, ALPHA/BETA, COMPLEX (INHIBITOR PROTEIN/KINASE)	COMPLEX (NHBITOR PROTEIN/KINASE) INHIBITOR PROTEIN, CYCLIN-DEPENDENT KINASE, CELL CYCLE 2 CONTROL,			
Coumpound	P19INK4D CDK4/6 INHIBITOR; CHAIN: NULL;	P19INK4D CDK4/6 INHIBITOR; CHAIN: NULL;	P19INK4D CDK4/6 INHIBITOR; CHAIN: NULL;	P19INK4D CDK4/6 INHIBITOR; CHAIN: NULL;	P19INK4D CDK4/6 INHIBITOR; CHAIN: NULL;	P19INK4D CDK4/6 INHIBITOR; CHAIN: NULL;	CYCLIN-DEPENDENT KINASE 6; CHAIN: A; P19INK4D; CHAIN: B;	CYCLIN-DEPENDENT KINASE 6; CHAIN: A; P19INK4D; CHAIN: B;	CYCLIN-DEPENDENT KINASE 6; CHAIN: A; P19INK4D; CHAIN: B;
SEQFOL D score								16 - <u>1</u>	
PMF score	0.49	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00
Verify	0.37	0.66	0.58	0.76	0.32	0.51	0.21	0.77	0.63
Psi Blast	4.86-10	4.5e-35	1.4e-40	1.5e-44	6e-42	1.5e-40	1.1e-36	3e-43	1.5e-41
END AA	574	605	637	673	739	805	610	673	743
STAR T AA	445	458	486	518	585	652	447	521	587
CHAI N ID		•		İ			В	æ	В
PDB ID	1bd8	15d8	15d8	8pq1	1 bd8	8pq1	1blx	1 b lx	16lx
SEQ ID NO:	1853	1853	1853	1853	1853	1853	1853	1853	1853

PDB annotation	ALPHA/BETA, COMPLEX (INHIBITOR PROTEIN/KINASE)	COMPLEX (INHIBITOR PROTEIN/KINASE) INHIBITOR	FROTEIN, CYCLIN-DEPENDENT KINASE, CELL CYCLE 2 CONTROL	ALPHA/BETA, COMPLEX (INHIBITOR PROTEIN/KINASE)	HORMONE/GROWTH FACTOR P18-	INK4C; CELL CYCLE INHIBITOR,	P18INK4C, TUMOR, SUPPRESSOR,	CYCLIN- 2 DEPENDENT KINASE, HORMONE/GROWTH FACTOR	HORMONE/GROWTH FACTOR P18-	INK4C; CELL CYCLE INHIBITOR,	P18INK4C, TUMOR, SUPPRESSOR,	CYCLIN- 2 DEPENDENT KINASE,	HORMONE/GROWTH FACTOR	TRANSFERASE CSK; PROTEIN	KINASE, C-TERMINAL SRC KINASE,	PHOSPHORYLATION, 2	SI AUROSPORINE, IKANSFERASE									SIGNALING PROTEIN HELIX-TURN-	HELIX, ANKYRIN REPEAT	SIGNALING PROTEIN HELIX-TURN-
Coumpound		CYCLIN-DEPENDENT KINASE 6; CHAIN: A; P19INK4D; CHAIN:	žá.		CYCLIN-DEPENDENT KINASE	6 INHIBITOR; CHAIN: A;			CYCLIN-DEPENDENT KINASE	6 INHIBITOR; CHAIN: A;				C-TERMINAL SRC KINASE;	CHAIN: A;			PHOSPHOIRANSFERASE	CAMP-DEFENDEN PROTEIN	KINASE CATALYTIC SUBUNIT	TO (1907) (1.37) CMR 4	I KANSFEKASE(PHOSPHOTRA	DEPENDENT PROTEIN VINASE	G C 2 2 1 2 2 (CAPK) 1 CTD 2	(CATALYTIC SUBUNITY ICTP 4	CYCLIN-DEPENDENT KINASE	4 INHIBITOR B; CHAIN: A;	CYCLIN-DEPENDENT KINASE
SEQFOL D score																	20,70	50.05			5	55.25						
PMF		. 1.90			0.87				1.00					0.98												1.00		1.00
Verify score		09:0			0.16	_			09.0					0.81												0.73		0.36
Psi Blast		4.5e-41			8e-09				4.5e-33					1.4e-45			1 5	1.5e-30			1 50 20	05-35.1				le-35		1,5e-33
END AA		808			576	an Komin			612					276			270	V + V			240	7#5				610		637
STAR T AA		651	-		444			,	486					24			-	-				+				478		510
CHAI N ID		щ			Ą				¥					∢			L.	ı)			D	<u> </u>				Ą		٧
PDB ID		1blx			1bu9		****		1bu9					loyg			1	YIIIS	***************************************		121		•			1d9s		1498
SEQ ID NO:		1853	- 10.01	and trade care to	1853				1853					1853			1052	107			1953	1077				1853		1853

PDB annotation	HELIX, ANKYRIN REPEAT	SIGNALING PROTEIN HELIX-TURN- HELIX, ANKYRIN REPEAT	SIGNALING PROTEIN HELIX-TURN-	HELIX, ANK YRIN REPEAT	SIGNALING PROTEIN HELIX-TURN-	HELIX, ANKYRIN REPEAT	SIGNALING PROTEIN HELIX-TURN-	METAI BRIDING DECTEN 2NIC	BRIDING MODITE ANEVENIA	REPEATS, METAL BINDING	PROTEIN	PHOSPHOTRANSFERASE FGFRIK,	FIBROBLAST GROWTH FACTOR	RECEPTOR 1; TRANSFERASE,	TYROSINE-PROTEIN KINASE, ATP-	BINDING, 2 PHOSPHORYLATION,	RECEPTOR,	PHOSPHOTRANSFERASE	PHOSPHOTRANSFERASE FGFRIK,	FIBROBLAST GROWTH FACTOR	RECEPTOR 1; TRANSFERASE,	TYROSINE-PROTEIN KINASE, ATP-	BINDING, 2 PHOSPHORYLATION,	RECEPTOR,	PHOSPHOTRANSFERASE	PHOSPHOTRANSFERASE FGFRIK,	FIBROBLAST GROWTH FACTOR	RECEPTOR 1; TRANSFERASE,	TYROSINE-PROTEIN KINASF ATP-	BINDING, 2 PHOSPHORYLATION,	RECEPTOR, PHOSPHOTRANSFERASE
Coumpound	4 INHIBITOR B; CHAIN: A;	CYCLIN-DEPENDENT KINASE 4 INHIBITOR B: CHAIN: A:	CYCLIN-DEPENDENT KINASE	4 INHIBITOR B; CHAIN: A;	CYCLIN-DEPENDENT KINASE	4 INHIBITOR B; CHAIN: A;	CYCLIN-DEPENDENT KINASE	PVK2. A SCOCIATED DROTEIN	BETA-CHAIN A.	W. William, China		FGF RECEPTOR 1; CHAIN: A, B;					•		FGF RECEPTOR 1; CHAIN: A, B;							FGF RECEPTOR 1; CHAIN: A, B;					
SEQFOL D score												114.87														112.87	inair-				
PMF score		1.00	1.00		1.00		0.92	0.51	;										1.00												
Verify score		59'0	0.36	9	0.43		0.54	0.13)										0.46												
Psi Blast		7.5e-38	9e-37		1.2e-34		36-34	4 50.32	1			1.5e-45				_			1.5e-45							7.5e-45	-				
END AA		673	743	500	773	1,0	807	694				293							276							292	•				
STAR T AA		545	809		545		677	513				18							×												
CHAI N ID		⊀	⊀		∢		€	A				¥							∢							m m					•
PDB ID		1d9s	1d9s	Ş	109S	99	10%	1dca	•			Ifgi							1fgk							ligk					
SEQ ID NO:		1853	1853	1050	1853		1853	1853				1853						1	1853						1	1853					

PDB annotation	PHOSPHOTRANSFERASE FGFRIK, FIBROBLAST GROWTH FACTOR RECEPTOR 1; TRANSFERASE, TYROSINE-PROTEIN KINASE, ATP- BINDING, 2 PHOSPHORYLATION, RECEPTOR, PHOSPHOTRANSFERASE	PHOSPHOTRANSFERASE C-SRC, P60-SRC, SRC, TYROSINE KINASE, PHOSPHORYLATION, SH2, SH3, 2 PHOSPHOTYROSINE, PROTOONCOGENE, PHOSPHOTRANSFERASE	TRANSFERASE P150, C-ABL; KINASE, KINASE INHIBITOR, STI- 571, ACTIVATION LOOP	PROTEIN KINASE CDK2; TRANSFERASE, SERINE/THREONINE PROTEIN KINASE, ATP-BINDING, 2 CELL CYCLE, CELL DIVISION, MITOSIS, PHOSPHORYLATION	CELL CYCLE INHIBITOR P18- INK4C(INK6); CELL CYCLE INHIBITOR, P18-INK4C(INK6), ANKYRIN REPEAT, 2 CDK 4/6 INHIBITOR	TRANSCRIPTION FACTOR P65; P50D; TRANSCRIPTION FACTOR, IKB/NFKB COMPLEX	TRANSCRIPTION FACTOR P65; P50D; TRANSCRIPTION FACTOR, IKB/NFKB COMPLEX
Coumpound	FGF RECEPTOR 1; CHAIN: A, B;	TYROSINE-PROTEIN KINASE SRC; CHAIN: NULL;	PROTO-ONCOGENE TYROSINE-PROTEIN KINASE ABL; CHAIN: A, B;	HUMAN CYCLIN-DEPENDENT KINASE 2; CHAIN: NULL;	CYCLIN-DEPENDENT KINASE 6 INHIBITOR; CHAIN: A, B;	NF-KAPPA-B P65 SUBUNIT; CHAIN: A; NF-KAPPA-B P50D SUBUNIT; CHAIN: C; I-KAPPA- B-ALPHA; CHAIN: D;	NF-KAPPA-B P65 SUBUNIT; CHAIN: A; NF-KAPPA-B P50D SUBUNIT; CHAIN: C; I-KAPPA-
SEQFOL D score		·		92.94			
PMF score	1.00	1.00	1.00		1.00	1.00	1.00
Verify score	0.50	0.79	0.51		0.36	0.41	0.41
Psi Blast	7.5e-45	1.2e-46	7.5e-45	9e-28	3e-34	4.5e-46	6e-53
END AA	276	276	276	326	809	647	089
STAR T AA	26	26	49	19	484	458	486
CHAI N ID	æ		Ą		4	D	Q
PDB ID	lfgk	1fmk	lfpu	Ihcl	lihb	likn	likn
SEQ ID NO:	1853	1853	1853	1853	1853	1853	1853

PDB annotation		ļ	IKB/NFKB COMPLEX	TRANSCRIPTION FACTOR P65;		INDINFINB COMPLEX	TRANSCRIPTION FACTOR P65;		- IKB/NFKB COMPLEX	A; COMPLEX	: (TRANSFERASE/SUBSTRATE)		TRANSDUCTION,	PHOSPHOTRANSFERASE, 2	COMPLEX (KINASE/PEPTIDE	SUBSTRATE/ATP ANALOG),	ENZYME, 3 COMPLEX	+			TYROSINE KINASE, SIGNAL	TRANSDUCTION,	PHOSPHOTRANSFERASE, 2	COMPLEX (KINASE/PEPTIDE	SUBSTRATE/ATP ANALOG),	ENZYME, 3 COMPLEX	(TRANSFERASE/SUBSTRATE)	ANK-REPEAT MYOTROPHIN,	TALVE AND AND AND AND AND AND AND AND AND AND
Coumpound	B-ALPHA; CHAIN: D;	NF-KAPPA-B P65 SUBUNIT; CHAIN: A; NF-KAPPA-B P50D	SUBUNIT; CHAIN: C; I-KAPPA- B-ALPHA; CHAIN: D;	NF-KAPPA-B P65 SUBUNIT;	CHAIN: A; NF-KAPPA-B P50D	SUBUINI ; CHAIN: C; 1-KAFFA- B-ALPHA; CHAIN: D;	NF-KAPPA-B P65 SUBUNIT;	CHAIN: A; NF-KAPPA-B P50D	SUBUNIT; CHAIN: C; I-KAPPA- B-ALPHA; CHAIN: D;	INSULIN RECEPTOR; CHAIN: A;	PEPTIDE SUBSTRATE; CHAIN:	Ä							INSULIN RECEPTOR; CHAIN: A;	PEPTIDE SUBSTRATE; CHAIN:	iii							MYOTROPHIN; CHAIN: NULL	
SEQFOL D score										114.32																			
PMF		1.00		1.00			1.00												3									0.93	_
Verify		0.21		0.26			0.15												0.65									0.46	
Psi Blast		85-99		4.5e-52			1.3e-54			1.5e-46	•							;	1.26-40			•						8e-13	
END		749		212			810			306								700	9/7									523	
STAR T AA		551		584			617			10								į	9									445	_
CHAI N ID		D		D			D			A	,	•							₹										
PDB ID		lika		lika			likn			lir3								;	CII.									1myo	
SEQ ID NO:		1853		1853			1853	-		1853								500,	1833									1853	

SEQ	PDB	CHAI	STAR	END	Psi Blast	Verify	PMF	SEQFOL	Coumpound	PDB annotation
a ë	a	a Z	1 AA	AA		score	score	D score		
										ACETYLATION, NMR, ANK-REPEAT
1853	1myo		461	589	8e-16	-0.06	0.46		MYOTROPHIN; CHAIN: NULL	ANK-REPEAT MYOTROPHIN, ACETYLATION, NMR, ANK-REPEAT
1853	1myo		521	635	4.5e-32	0.55	1.00	,	MYOTROPHIN; CHAIN: NULL	ANK-REPEAT MOOTESPHIN,
1853	lmyo	•	554	699	1.5e-36	0.44	1.00		MYOTROPHIN; CHAIN; NULL	ANK-REPEAT MYOTROPHIN,
020.			į			,	,			ACETYLATION, NMR, ANK-REPEAT
1853	Imyo		621	735	1.5e-32	0.34	0.99		MYOTROPHIN, CHAIN: NULL	ANK-REPEAT MYOTROPHIN, ACETYLATION, NMR. ANK-REPEAT
1853	1myo		654	292	3e-33	-0.03	0.57		MYOTROPHIN; CHAIN: NULL	ANK-REPEAT MYOTROPHIN,
1853	lmvo		684	800	1.5e-30	0.37	8		MVOTROPHIN: CHAIN: NIII I	ANK DEBEAT MYOTEODEM
)		-	3	22.20	, ,	20:1		MI OTHER THEIR MODE	ACETYLATION, NMR, ANK-REPEAT
1853	Jufi	四	194	637	6e-43	0.50	1.00		NF-KAPPA-B P65; CHAIN: A, C;	COMPLEX (TRANSCRIPTION
									NF-KAPPA-B P50; CHAIN: B, D;	REG/ANK REPEAT) COMPLEX
									I-KAPPA-B-ALPHA; CHAIN: E,	(TRANSCRIPTION
									Ŧ.	REGULATION/ANK REPEAT),
										ANKYRIN 2 REPEAT HELIX
1853	Infi	ш	484	677	3e-50	0.52	1.00		NF-KAPPA-B P65; CHAIN: A, C;	COMPLEX (TRANSCRIPTION
									NF-KAPPA-B P50; CHAIN: B, D;	REG/ANK REPEAT) COMPLEX
									I-KAPPA-B-ALPHA; CHAIN: E,	(TRANSCRIPTION
									ġ,	REGULATION/ANK REPEAT),
52.00		ļ	9.	4,4						ANKYKIN 2 KEPEAT HELIX
1855		1)	249	749	1.2e-53	0.54	9:1		NF-KAPPA-B P65; CHAIN: A, C;	COMPLEX (TRANSCRIPTION
******					•				NF-KAPPA-B P50; CHAIN: B, D;	REG/ANK REPEAT) COMPLEX
		• • •						• •	I-KAPPA-B-ALPHA; CHAIN: E,	(TRANSCRIPTION
		_					:		ŭ	REGULATION/ANK REPEAT),
										ANKYRIN 2 REPEAT HELIX
1853	担	ш	581	778	1.5e-53	0.20	1.00		NF-KAPPA-B P65; CHAIN: A, C;	COMPLEX (TRANSCRIPTION
									NF-KAPPA-B P50; CHAIN: B, D;	REG/ANK REPEAT) COMPLEX
									I-KAPPA-B-ALPHA; CHAIN: E,	(TRANSCRIPTION
			**********						ij.	REGULATION/ANK REPEAT),
1053	4	r.			2				2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	ANKYRIN 2 REPEAT HELIX
165		T]	010	815	1.3e-33	0.26	1.00		NF-KAPPA-B P65; CHAIN: A, C;	COMPLEX (TRANSCRIPTION

PDB annotation	REG/ANK REPEAT) COMPLEX (TRANSCRIPTION REGULATION/ANK REPEAT), ANKYRIN 2 REPEAT HELIX	TRANSFERASE MITOGEN ACTIVATED PROTEIN KINASE; TRANSFERASE, MAP KINASE, SERINE/THREONINE-PROTEIN KINASE, 2 P38	TRANSFERASE MAP KINASE, SERINE/THREONINE PROTEIN KINASE, TRANSFERASE	TYROSINE KINASE TYROSINE KINASE-INHIBITOR COMPLEX, DOWN-REGULATED KINASE, 2 ORDERED ACTIVATION 1 OOP	TRANSFERASE ALPHA BETA FOLD	TRANSCRIPTION REGULATION TRANSCRIPTION REGULATION, ANKYRIN REPEATS. CELL-CYCLE	TRANSCRIPTION REGULATION TRANSCRIPTION REGULATION ANKYRN REPEATS CELL CYCLE	COMPLEX (ANTI- COMPLEX (ANTI- CONCOGENE/ANKYRIN REPEATS) P33BP2; ANKYRIN REPEATS, SH3, P33, TUMOR SUPPRESSOR, MULTIGENE 2 FAMILY, NUCLEAR PROTEIN, PHOSPHORYLATION, DISEASE MULTATION, 3 POLYMORPHISM, COMPLEX (ANTI- ONCOGENE/ANKYRIN PEPEATS)	COMPLEX (ANTI- ONCOGENE/ANKYRIN REPEATS)
Coumpound	NF-KAPPA-B P50; CHAIN: B, D; I-KAPPA-B-ALPHA; CHAIN: E, F;	MAP KINASE P38; CHAIN: NULL;	ERK2; CHAIN: NULL;	HAEMATOPOETIC CELL KINASE (HCK); CHAIN: A;	LCK KINASE: CHAIN: A:	REGULATORY PROTEIN SWI6; CHAIN: A, B;	REGULATORY PROTEIN SW16; CHAIN: A, B;	P53; CHAIN: A; 53BP2; CHAIN: B;	P53; CHAIN: A; 53BP2; CHAIN: B;
SEQFOL D score		92.67	97.49						
PMF score				1.00	1.80	0.10	0.00	96.0	1.00
Verify score	,	·		0.66	0.71	-0.40	-0.17	0.27	0.31
Psi Blast		3e-27	6e-29	1.5e-49	7.5e-50	1.5e-17	1.5e-40	3.2e-12	6.4e-12
END AA		359	358	276	276	592	759	503	578
STAR T AA		4	15	26	26	466	512	452	458
CHAI N ID				∢	A	A	₹,	ш	М
PDB ID		1p38	Ipme	Iqof	1qpc	lsw6	1sw6	1ycs	lycs
SEQ ID NO:		1853	1853	1853	1853	1853	1853	1853	1853

PDB annotation	P53BP2; ANKYRIN REPEATS, SH3, P53, TUMOR SUPPRESSOR, MULTIGENE 2 FAMILY, NUCLEAR PROTEIN, PHOSPHORYLATION, DISEASE MUTATION, 3 POLYMORPHISM, COMPLEX (ANTI-			
Coumpound		P53; CHAIN: A; 53BP2; CHAIN: B;	P53; CHAIN: A; 53BP2; CHAIN: B;	P53; CHAIN: A; 53BP2; CHAIN: B;
SEQFOL D score			1 25	
PMF		0.99	66.0	0.30
Verify score		0.09	0.26	-0.13
Psi Blast		6e-33	1.4e-38	7.5e-33
END		099	726	608
STAR T AA		488	554	654
CHAI N ID		m	м	æ
PDB ID		lycs	1 yes	lycs
SEQ ID NO:		1853	1853	1853

				T	·	1	
PDB annotation	TRANSFERASE MITOGEN ACTIVATED PROTEIN KINASE, MAP 2, ERK2; TRANSFERASE, SERINE/THREONINE-PROTEIN KINASE, MAP KINASE, 2 ERK2	SIGNALING PROTEIN GTP-BINDING PROTEINS, PROTEIN-PROTEIN COMPLEX, EFFECTORS	SIGNALING PROTEIN GTP-BINDING PROTEINS, PROTEIN-PROTEIN COMPLEX, EFFECTORS	SIGNALING PROTEIN G PROTEIN, GTP HYDROLYSIS, KINETIC CRYSTALLOGRAPHY, 2 SIGNALING PROTEIN	SIGNALING PROTEIN G PROTEIN, GTP HYDROLYSIS, KINETIC CRYSTALLOGRAPHY, 2 SIGNALING PROTEIN	ENDOCYTOSIS/IEXCE-1-OSIS G- PROTEIN, GTPASE, RAB6, VESICULAR TRAFFICKING	SIGNALING PROTEIN P21-RAC2; RHO GDI 2, RHO-GDI BETA, LY-GDI; BETA SANDWHICH, PROTEIN- PROTEIN COMPLEX, G-DOMAIN, 2 IMMUNOGLOBULIN FOLD, WALKER FOLD, GTP-BINDING
Coumpound	EXTRACELLULAR REGULATED KINASE 2; CHAIN: NULL;	RAS-RELATED PROTEIN RAP- 1A; CHAIN: A; PROTO- ONKOGENE SERINE/THREONINE PROTEIN KINASE CHAIN: B:	RAS-RELATED PROTEIN RAP- 1A; CHAIN: A; PROTO- ONKOGENE SERINE/THREONINE PROTEIN KINASE CHAIN: B;	TRANSFORMING PROTEIN P21/H-RAS-1; CHAIN: A;	TRANSFORMING PROTEIN P21/H-RAS-1; CHAIN: A;	RAB6 GTPASE; CHAIN: A;	RAS-RELATED C3 BOTULINUM TOXIN SUBSTRATE 2; CHAIN: A; RHO GDP-DISSOCIATION INHIBITOR 2; CHAIN: B;
SEQFOL D score	107.86	85.26			77.02		
PMF score			007	1.00		1.00	0.59
Verify score			0.43	0.55		0.48	0.12
Psi Blast	9e-31	9.6e-68	9.6e-68	1.6e-68	1.6e-68	6.4e-56	3.2e-53
END AA	356	171	173	173	174	171	176
STAR T AA	w	-		1		3	1
CHAI N ID		A	Ą	Ą	¥	Ą	¥
PDB ID	3erk	lcly	lcly	letq	lctq	1d5c	9sp1
SEQ ID NO:	1853	1854	1854	1854	1854	1854	1854

PDB annotation	ENDOCYTOSIS/EXOCYTOSIS G PROTEIN, VESICULAR TRAFFIC, GTP HYDROLYSIS, YPT/RAB 2 PROTEIN, ENDOCYTOSIS, HYDROLASE	GTP-BINDING PROTEIN GTP- BINDING PROTEIN, SMALL G PROTEIN, RAP, GDP RAS	GTP-BINDING PROTEIN GTP- BINDING PROTEIN, SMALL G PROTEIN, RAP2, GIDP. RAS	GTP-BINDING GTP-BINDING, GTPASE, SMALL G-PROTEIN, RHO FAMILY RAS SIPPER 2 FAMILY	GTP-BINDING GENERALING GTP-BASE, SMALL G-PROTEIN, RHO FAMILY, RAS SUPER 2 FAMILY.		COMPLEX (SMALL GTPASENUCLEAR PROTEIN) COMPLEX (SMALL GTPASENUCLEAR PROTEIN), SMALL GTPASE, 2 NUCLEAR	COMPLEX (GTP- BINDING/EFFECTOR) RAS-RELATED PROTEIN RAB3A; COMPLEX (GTP-
Coumpound	GTP-BINDING PROTEIN YPT51; BY CHAIN: A; PR	RAP2A; CHAIN: NULL; GI	RAP2A; CHAIN: NULL; GT BI PR	RAC1; CHAIN: NULL; GT GT	RACI; CHAIN: NULL; G1 G1 PA	ν. 44	RAN; CHAIN: A, C; NUCLEAR CC PORE COMPLEX PROTEIN GT NUP358; CHAIN: B, D; CC GT SIM	RAB-3A; CHAIN: A; CC RABPHILIN-3A; CHAIN: B; BII
SEQFOL D score	·		95.27	52.65			50.36	60.15
PMF score	00.1	1.00			0.94	1.00		
Verify score	0.31	0.49			0.28	0.37		
Psi Blast	6.4e-55	4.8e-64	4.8e-64	1.1e-53	1.1e-53	4.8e-52	4.8e-36	8e-59
END	174	121	174	174	176	171	186	179
STAR T AA	,	_	-	-	2		7	-
CHAI N ID	Ą				•		ນ	∢
PDB ID	lek0	Ikao	1kao	1mh1	Imh1		क्या	Izbd
SEQ ID NO:	1854	1854	1854	1854	1854	1854	828	1854

						
PDB annotation	BINDING/EFFECTOR), G PROTEIN, EFFECTOR, RABCDR, 2 SYNAPTIC EXOCYTOSIS, RAB PROTEIN, RAB3A, RABPHILIN	COMPLEX (GTP-BINDING) RAS-RELATED BINDING/EFFECTOR) RAS-RELATED PROTEIN RABSA, COMPLEX (GTP-BINDING/EFFECTOR), G PROTEIN, EFFECTOR, RABCDR, 2 SYNAPTIC EXOCYTOSIS, RAB PROTEIN, RABSA, RABPHILIN	HYDROLASE CDC42/CDC42GAP; CDC42/CDC42GAP; TRANSITION STATE, G-PROTEIN, GAP, CDC42, ALF3 HYDROLASE	HYDROLASE G PROTEIN, VESICULAR TRAFFICKING, GTP HYDROLYSIS, RAB 2 PROTEIN, NEUROTRANSMITTER RELEASE, HYDROLASE	HYDROLASE G PROTEIN, VESICULAR TRAFFICKING, GTP HYDROLYSIS, RAB 2 PROTEIN, NEUROTRANSMITTER RELEASE, HYDROLASE	COMPLEX (SERINE PROTEASE/INHIBITOR) SKIN- DERIVED ANTILEUKOPROTEINASE (SKALP); HYDROLASE, SERINE PROTEASE, 3D-STRUCTURE, ZYMOGEN, PANCREAS, 2 SIGNAL, COMPLEX (SERINE PROTEASE/INHIBITOR)
Соитроньа		RAB-3A; CHAIN: A; RABPHILIN-3A; CHAIN: B;	GTP BINDING PROTEIN (G25K); CHAIN: A; GTPASE ACTIVATING PROTEIN (RHG); CHAIN: B;	RAB3A; CHAIN: A;	RAB3A; CHAIN: A;	ELASTASE; CHAIN: E; ELAFIN; CHAIN: 1;
SEQFOL D score			54.33	68.59		
PMF score		0.96			0.99	0.48
Verify score		0.43	, 11		0.27	-0.71
Psi Blast		8e-59	3.2e-50	1.1e-59	1.1e-59	3.2e-16
END		176	193	174	174	72
STAR T AA		4	-	. 2	য	23
CHAI		•	⋖	¥	4	provide
PDB ID		1zbd	Zngr	3rab	3rab	Iffe
SEQ B B		1854	1854	1854	1854	1856

PDB CI		CHAI	STAR T AA	END	Psi Blast	Verify score	PMF	SEQFOL D score	Coumpound	PDB approximate
ligr A	¥	•	32	08	0.0011	-0.54	0.12		INSULIN-LIKE GROWTH FACTOR RECEPTOR 1; CHAIN: A:	HORMONE RECEPTOR HORMONE RECEPTOR, INSULIN RECEPTOR FAMILY
2rel			30	72	1.5e-17	-0.02	0.46		R-ELAFIN; CHAIN; NULL;	SERINE PROTEASE INHIBITOR SERINE PROTEASE INHIBITOR, R- ELAFIN, ELASTASE INHIBITOR
lc1y A	₹		19	177	9.6e-25			50.43	RAS-RELATED PROTEIN RAP- 1A; CHAIN: A; PROTO- ONKOGENE SERINE/THREONINE PROTEIN KINASE CHAIN: B:	SIGNALING PROTEIN GTP-BINDING PROTEINS, PROTEIN-PROTEIN COMPLEX, EFFECTORS
lcxz A	∢		ឧ	185	1.6e-28	-0.14	0.01		HIS-TAGGED TRANSFORMING PROTEIN RHOA(0-181); CHAIN: A: PKN: CHAIN: B:	SIGNALING PROTEIN PROTEIN- PROTEIN COMPLEX, ANTIPARALLEL COILED-COIL
1d5c A	<		21	183	3.2e-30	-0.22	0.01		RAB6 GTPASE; CHAIN: A;	ENDOCYTOSIS/EXOCYTOSIS G- PROTEIN, GTPASE, RAB6, VESICULAR TRAFFICKING
le0s A	4		14	191	4.8e-52	0.11	1.00		ADP-RIBOSYLATION FACTOR 6; CHAIN: A;	G PROTEIN G PROTEIN, RAS, ARF, ARF6, MEMBRANE TRAFFIC
lek0 A	∢		22	183	3.26-28	0.06	-0.13		GTP-BINDING PROTEIN YPT51; CHAIN: A;	ENDOCYTOSIS/EXOCYTOSIS G PROTEIN, VESICULAR TRAFFIC, GTP HYDROLYSIS, YPT/RAB 2 PROTEIN, ENDOCYTOSIS, HYDROLASE
lfzq A	≺		7	190	1.1e-48	0.50	1.00		ADP-RIBOSYLATION FACTOR. LIKE PROTEIN 3; CHAIN: A;	SIGNALING PROTEIN ARF-LIKE PROTEIN 3, ARL3; PROTEIN-GDP COMPLEX WITHOUT MAGNESIUM, ARF FAMILY, RAS 2 SUPERFAMILY, G-DOMAIN
1hur A	4		9	182	6.4e-57			83.99	HUMAN ADP-RIBOSYLATION FACTOR 1; IHUR 5 CHAIN: A, B; IHUR 7	PROTEIN TRANSPORT GDP. BINDING, MEMBRANE TRAFFICKIN, NON-MYRISTOYLATED IHUR 16
1hur A	∢		9	192	6.4e-57	0.23	0.92		HUMAN ADP-RIBOSYLATION	PROTEIN TRANSPORT GDP-

PDB annotation	BINDING, MEMBRANE TRAFFICKIN, NON-MYRISTOYLATED 1HUR 16	GTP-BINDING PROTEIN GTP- BINDING PROTEIN, SMALL G PROTEIN, RAP2, GDP, RAS	COMPLEX(GTPASE ACTIVATIN/PROTO-ONCOGENE) GTPASE-ACTIVATING PROTEIN RHOGAP; COMPLEX (GTPASE ACTIVATION/PROTO-ONCOGENE), GTPASE, 2 TRANSITION STATE, GAP	HYDROLASE GPROTEIN, VESICULAR TRAFFICKING, GTP HYDROLYSIS, RAB 2 PROTEIN, NEUROTRANSMITTER RELEASE, HYDROLASE		COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING	PROTEIN	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
Coumpound	FACTOR 1; IHUR 5 CHAIN: A, B; IHUR 7	RAP2A; CHAIN: NULL;	P50-RHOGAP; CHAIN: A; TRANSFORMING PROTEIN RHOA; CHAIN: B;	RAB3A; CHAIN: A;		QGSR ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING	SITE; CHAIN: B, C;	QGSR ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	QGSR ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING SITE: CHAIN: B. C:	DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;
SEQFOL D score		50.54						58.29		
PMF			-0.03	0.30		0.28			0.51	0.09
Verify score	, ,		0.22	-0.03		-0.07			0.40	-0.22
Psi Blast		1.6e-24	1.6e-27	3.2e-33		3.2e-30		3.2e-31	3.2e-31	3.2e-50
END		186	185	190		132		162	160	188
STAR T AA		19	8 2	22		52		76	08	107
CHAI N ID			Д	¥		¥		¥	Y	U
PDB ID		1kao	1tx4	3rab		Ialh		lalh	laih	lmey
SEQ UO:		1857	1857	1857		1858		1858	1858	1858

PDB annotation	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)	COMPLEX (TRANSCRIPTION REGULATION/DNA) TFIIIA; 5S GENE; NMR, TFIIIA, PROTEIN, DNA, TRANSCRIPTION FACTOR, 5S RNA 2 GENE, DNA BINDING PROTEIN, ZINC FINGER, COMPLEX 3 (TRANSCRIPTION REGULATION/DNA)	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG I; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YYJ, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-
Coumpound	DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	TRANSCRIPTION FACTOR IIIA; CHAIN: A; SS RNA GENE; CHAIN: E, F;	YY1; CHAIN: C; ADENO- ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	ZINC FINGER PROTEIN GLII; CHAIN: A; DNA; CHAIN: C, D;
SEQFOL D seore			62.32			
PMF score	0.17	0.98		0.24	0.39	0.10
Verify score	-0.18	0.17		0.14	80.0-	-0.10
Psi Blast	4.8e-50	1.4e-50	I,4e-50	3.2e-20	1.3e-34	3.2e-33
END	132	160	191	160	160	162
STAR T AA	51	79	79	08	95	11
CHAI N ID	ပ	Ü	င	A	•	Ą
PDB ID	Imey	1mey	lmey	1453	lubd	2gli
SEQ ID NO:	1858	1858	1858	1858	1858	1858

	PDB ID	CHAI N ID	STAR T AA	END AA	Psi Blast	Verify	PMF	SEQFOL D score	Coumpound	PDB annotation
	-		;							BINDING PROTEIN/DNA)
	Zg11	e	51	188	4.8e-34			58:21	ZINC FINGER PROTEIN GLII; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
	2gli	¥	53	881	4.8e-34	-0.37	0.11		ZINC FINGER PROTEIN GLII; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
\pm										
	la]h	V	Z.	198	6.4e-29			60.10	QGSR ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING SITE: CHAIN: B. C:	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTFIN
	lalb	4	117	197	6.4e-29	-0.04	0.78		QGSR ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING
+			,;;	100					SILE; CHAIN: B, C;	PROTEIN
	lain	4	145	237	4.8e-27	-0.23	0.35		QGSR ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN
	laih	Ą	212	273	6.4e-15	0.07	-0.13		OGSR ZINC FINGER PEPTIDE:	COMPLEX (ZINC FINGER/DNA)
—					**************************************				CHAIN: A; DUPLEX	COMPLEX (ZINC FINGER/DNA),
									OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	ZINC FINGER, DNA-BINDING PROTEIN
	dlal	V	%	169	3.2e-25	-0.26	0.10		QGSR ZINC FINGER PEPTIDE;	COMPLEX (ZINC FINGER/DNA)
								•	CHAIN: A; DUPLEX	COMPLEX (ZINC FINGER/DNA),
									OLIGONOCLEOTIDE BINDING SITE; CHAIN: B, C;	ZINC FINGER, DNA-BINDING PROTEIN
	Imey	ပ	116	197	1.6e-50	-0.03	1.00		DNA; CHAIN: A, B, D, E;	COMPLEX (ZINC FINGER/DNA) ZINC
	***								CONSENSUS ZINC FINGER	FINGER, PROTEIN-DNA
									PROTEIN; CHAIN: C, F, G;	INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX

	PDB annotation	(ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA) ZINC	FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN-DESTGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)	
	Coumpound	DNA; CHAIN: A, B, D, E;	CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	TRANSCRIPTION REGULATION YEAST TRANSCRIPTION FACTOR ADRI (RESIDUES 130-
	SEQFOL D score	70.79		:17 , 7					, -
	PMF score			0.43	0.12	0.00	0.35	0.42	0.81
	Verify			-0.02	-0.35	-0.22	-0.10	-0.11	-0.29
nge i silita angi ma	Psi Blast	1.6e-50		1.3e-46	1.1e-33	1.4e-26	1.16-41	1.4e-11	8e-06
	END	198		237	265	141	169	237	239
	STAR T AA	116		144	172	85	88	209	212
	CHAI N ID	O		٠ ن	ن ن	ပ	၁	<u>ت</u> .	
	PDB ID	lmey		Imey	Imey	Іпеу	lmey	Imey	lpaa
	SEQ NO:	1859		1859	1859	1859	1859	1859	1859

PDB annotation) S	ZINC FINGER TRANSCRIPTION FACTOR SP1; ZINC FINGER, TRANSCRIPTION ACTIVATION, SP1	COMPLEX (TRANSCRIPTION REGULATION/DNA) TFIIIA; 5S GENE; NWR, TFIIIA, PROTEIN, DNA, TRANSCRIPTION FACTOR, 5S RNA 2 GENE, DNA BINDING PROTEIN, ZINC FINGER, COMPLEX 3 (TRANSCRIPTION REGULATION/DNA)	COMPLEX (TRANSCRIPTION REGULATION/DNA) TFIIIA; 5S GENE; NMR, TFIIIA, PROTEIN, DNA, TRANSCRIPTION FACTOR, 5S RNA 2 GENE, DNA BINDING PROTEIN, ZINC FINGER, COMPLEX 3 (TRANSCRIPTION REGULATION/DNA)	COMPLEX (TRANSCRIPTION REGULATION/DNA) TFIIIA; 5S GENE; NMR, TFIIIA, PROTEIN, DNA, TRANSCRIPTION FACTOR, 5S RNA 2 GENE, DNA BINDING PROTEIN, ZINC FINGER, COMPLEX 3 (TRANSCRIPTION
Coumpound	159) IPAA 3 (PAPA - CARBOXY TERMINAL ZINC FINGER DOMAIN) MUTANT WITH IPAA 4 PRO 131 REPLACED BY ALA, PRO 133 REPLACED BY ALA, CYS 140 IPAA 5 REPLACED BY ALA (P131A,P133A,C140A) (NMR, 10 STRUCTURES) IPAA 6	SPIF2; CHAIN: NULL;	TRANSCRIPTION FACTOR IIIA; CHAIN: A; SS RNA GENE; CHAIN: E, F;	TRANSCRIPTION FACTOR IIIA; CHAIN: A; SS RNA GENE; CHAIN: E, F;	TRANSCRIPTION FACTOR IIIA; CHAIN: A; 58 RNA GENE; CHAIN: E, F;
SEQFOL D score				55.20	1
PMF score		0.03	0000		0.48
Verify score		-0.25	-0.52		-0.08
Psi Blast		3.2e-05	1.16-16	1.4e-20	1.46-20
END		. 239	169	201	198
STAR T AA		212	105	114	117
CHAI N ID	•		∢	Ą	ď
PDB ID		1sp2	1153	1ft3	145
SEQ ID NO:		1859	1859	1859	1859

	_			-				_											_			_				
PDB annotation	REGULATION/DNA)	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX	(IRANSCRIPTION REGULATION/DNA), RNA	POLYMERASE III, 2	TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN	COMPLEX (TRANSCRIPTION REGILLATION/DNA) COMPLEX	(TRANSCRIPTION	REGULATION/DNA), RNA	POLYMERASE III, 2	TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN	COMPLEX (TRANSCRIPTION	REGULATION/DNA) COMPLEX	PEGIT ATIONAL PNA	POLYMERASE III. 2	TRANSCRIPTION INITIATION ZINC	FINGER PROTEIN	COMPLEX (TRANSCRIPTION	REGULATION/DNA) COMPLEX	(IKANSCKIPTION	POI VAGERANE III 2	TRANSCRIPTION INITIATION, ZINC	FINGER PROTEIN	COMPLEX (TRANSCRIPTION	REGULATION/DNA) YING-YANG 1;	INITIATOR ELEMENT, YY1, ZINC 2	FINGER PROTEIN, DNA-PROTEIN
Coumpound		TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE;	CHAIN: B, C, E, F;			TFIIIA; CHAIN; A, D; 5S RIBOSOMAI, RNA GENE:	CHAIN: B, C, E, F;				TFIIIA; CHAIN: A, D; 5S	RIBOSOMAL RNA GENE;	CIMIN: 43, C, E, 13				TFIIIA; CHAIN: A, D; 5S	RIBOSOMAL RNA GENE;	CHAIN: B, C, E, F;				YY1; CHAIN: C; ADENO-	ASSOCIATED VIRUS PS INITIATOR RIFMENT DNA:	CHAIN: A, B;	
SEQFOL D score							,				98.99															
PMF score		0.10				0.33											0.01						0,45			
Verify score		-0.24				-0.01											-0.25						-0.00			
Psi Blast		1.4e-28				1.1e-28					1.1e-28						3.2e-16						3e-22			
END		239				275					237	-, -					178						220			
STAR T AA		105				117					50				1-47		98						011			
CHAI N ID		Ą				¥	a-mor - k				A						¥						C			
PDB ID		1466				1476			···		1tf6	<u></u>					1tf6						lubd			
SEQ ID NO:		1859				6581					1859						1859.						6581			

WO 02/070539 PCT/US02/05095

PDB annotation	RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1;	TRANSCRIPTION INITIATION, INITIATOR BY EMENT VV1 21NC 2	FINGER PROTEIN, DNA-PROTEIN	RECOGNITION, 3 COMPLEX (TRANSCRIPTION	REGULATION/DNA)	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1;	TRANSCRIPTION INITIATION,	INITIATOR ELEMENT, YY1, ZINC 2	PECCENTION 3 COMPLEY	(TRANSCRIPTION	(REGULATION/DNA)	COMPLEX (TRANSCRIPTION	REGULATION/DNA) YING-YANG 1;	TRANSCRIPTION INITIATION,	INITIATOR ELEMENT, YY1, ZINC 2	FINGER PROTEIN, DNA-PROTEIN	RECOGNITION, 3 COMPLEX	(TRANSCRIPTION	REGULATION/DNA)	TRANSCRIPTION REGULATION	INAMOCAL HOM KEGULA HOM,	ADKI, ZINC FINGER, INMR	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI;	GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
Coumpound		YY1; CHAIN: C; ADENO- ASSOCIATED VIRUS P5	INITIATOR ELEMENT DNA;	CLIMIN: A, B,			YY1; CHAIN: C; ADENO- ASSOCIATED VIRUS P5	INITIATOR ELEMENT DNA;	CHAIN: A, B;				YY1; CHAIN: C; ADENO-	ASSOCIATED VIRUS PS	INITIATOR ELEMENT DNA;	CHAIN: A, B;				-	ADRI; CHAIN: NULL;			ZINC FINGER PROTEIN GLII; CHAIN: A; DNA; CHAIN: C, D;	
SEQFOL D score						•	68.47			•															
PMF	-	0.07				_							86.0								0.37			0.33	·
Verify score		-0.06											-0.27								-0.05			-0.22	
Psi Blast		3.2e-22					3.2e-33						3.2e-33								3.2e-16			6.4e-33	
END AA		265		-			861						197								171		,	66I	
STAR T AA		152					%						93								117			90	
CHAI N ID		၁					ပ		•				ပ										1	∢	
PDB ID		1ubd		_			lubd						1 ubd					•	****		2adr			2g11	
SEQ ID NO:		1859					1859						1859								1859		3	1859	

PDB annotation	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA- BINDING PROTEIN/DNA)	COMPLEX (ZINC FINGER/DNA)	COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING	FROIEIN	COMPLEX (ZINC FINGER/DNA)	COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING	PROTEIN	COMPLEX (ZINC FINGER/DNA)	COMPLEA (ZINC FINGER/DIA),	ZINC FINGER, DINA-BINDING PROTEIN	GENE REGULATION POZ DOMAIN;	PROTEIN-PROTEIN INTERACTION	REPRESSOR, ZINC-FINGER	PROTEIN, X-RAY	CRYSTALLOGRAPHY, 3 PROTEIN	STRUCTURE, PROMYELOCYTIC	GENE REGILLATION POZ DOMAIN:	PROTEIN-PROTEIN INTERACTION	DOMAIN, TRANSCRIPTIONAL 2	REPRESSOR, ZINC-FINGER PROTEIN, X-RAY
Coumpound	ZINC FINGER PROTEIN GLII; CHAIN: A; DNA; CHAIN: C, D;	ZINC FINGER PROTEIN GLII; CHAIN: A; DNA; CHAIN: C, D;	OGSR ZINC FINGER PEPTIDE:	CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING	SILE; CERMIN: B, C;	OGSR ZINC FINGER PEPTIDE;	CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING	SITE; CHAIN: B, C;	QGSR ZINC FINGER PEPTIDE;	CHAIN: A; DUPLEA	SITE; CHAIN: B, C;	PROMYELOCYTIC LEUKEMIA	ZINC FINGER PROTEIN PLZF;	CIMIN: A,				PROMYEL OCYTIC LELIKEMIA	ZINC FINGER PROTEIN PLZF;	CHAIN: A;	
SEQFOL D score	68.84					69.01												64.40			
PMF score		0.04	1.00						0.41			1.00									
Verify score		0.04	0.37						-0.35			0.40									
Psi Blast	6.4e-33	1.3e-3.1	4.8e-32		,	4.8e-32	,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,		3.2e-28			1.3e-37						1.3e-37	•		
END AA	238	237	452			453			488		_	126						126			
STAR T AA	83	96	371			372			399			4	ما المام موران والوا					S			
CHAI N ID	Ą	¥	A			A			A			¥			•			A			
PDB ID	2gli	2gli	laih			laIh			lalh			Ibuo						1buo			
SEQ ID NO:	1859	1859	1860			1860			1860			1860						1860			

	PDB annotation	CRYSTALLOGRAPHY, 3 PROTEIN STRUCTURE, PROMYELOCYTIC LEUKEMIA, GENE REGULATION	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)	COMPLEX (TRANSCRIPTION REGULATION/DNA) TFIIIA; SS GENE; NMR, TFIIIA, PROTEIN, DNA, TRANSCRIPTION FACTOR, 5S RNA 2 GENE, DNA BINDING PROTEIN, ZINC FINGER, COMPLEX 3 (TRANSCRIPTION REGULATION/DNA)	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION
	Coumpound		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	TRANSCRIPTION FACTOR IIIA; CHAIN: A; SS RNA GENE; CHAIN: E, F;	TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;
	SEQFOL D score				67.59			
	PMF		60.09	1.00		0.71	0.23	0.11
การเก็บสู่เล่าการเพิ่มได้เรียก -	Verify score	v.afi.	-0.44	0.14		-0.16	-0.48	-0.38
e Capacita de La Marijanja	Psi Blast		1.6e-47	1.3e-50	1.3e-50	3.2e-47	3.2e-19	1.6e-31
	END AA	,	423	452	452	488	488	490
	STAR T AA		336	370	370	398	399	371
	CHAI N ID		S	ပ	0	၁	¥	А
	PDB TD		Ітеу	lmey	lmey	lmey	9	1tf6
	SEQ ID NO:		1860	1860	1860	1860	1860	1860

						Γ
PDB annotation	REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN	COMPLEX (TRANSCERFICON - REGULATION/DNA) YING-YANG I; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YYI, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG I; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA- BINDING PROTEIN/DNA)	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI:
Coumpound		YYI; CHAIN: C; ADENO- ASSOCIATED VIRUS PS INITIATOR ELEMENT DNA; CHAIN: A, B;	YYI; CHAIN: C; ADENO- ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	YYI; CHAIN: C; ADENO- ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	ZINC FINGER PROTEIN GLII; CHAIN: A; DNA; CHAIN: C, D;	ZINC FINGER PROTEIN GLII; CHAIN: A: DNA; CHAIN; C. D;
SEQFOL D score						
PMF		0.92	0.89	0.10	-0.20	0.07
Verify score		-0.05	-0.03	-0.08	0.05	0.10
Psi Blast		1.1e-32	6.4e-34	4.8e-24	1.6e-09	6.4e-34
END AA		8448	488	493	313	452
STAR T AA		344	375	406	224	319
CHAI N ID		•	ပ	ပ	¥	Ą
PDB ID		pqn1	pqnI	lubd	2gli	2gli
SEQ ID NO:		1860	1860	1860	1860	1860

Coumpound PDB annotation	GLI, ZINC FINGER, COMPLEX (DNA- BINDING PROTEIN/DNA)	ZINC FINGER PROTEIN GL11; CHAIN: A; DNA; CHAIN: C, D; GL1, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA) BINDING PROTEIN/DNA)	DNA NÜCLEOTIDE EXCISION REPLICATION DNA NÜCLEOTIDE REPAIR ENZYME UVRB; EXCISION REPAIR, UVRABC, HELICASE. 2	EXCINUCLEASE ABC SUBUNIT HYDROLASE UVRB; MULTIDOMAIN B; CHAIN: A;	EXCINUCLEASE ABC SUBUNIT HYDROLASE UVRB; MULTIDOMAIN B; CHAIN: A;	EXCINUCLEASE UVRABC COMPONENT UVRB; CHAIN: A;	EUKARYOTIC INITIATION TRANSLATION YEAST INITIATION	FACTOR 4A; CHAIN: A; FACTOR 4A, EIF4A; HELICASE, INITIATION FACTOR 4A, DEAD-BOX PROTEIN	ON FACTOR	HELICASE, DEAD-BOX PROTEIN	YEAST INITIATION FACTOR TRANSLATION EUKARYOTIC 4A; CHAIN: A, B; INTIATION FACTOR 4A; IF4A, HFI ICASE DEAD-ROX PROTEIN	GTP-BINDING PROTEIN RAN; TRANSPORT PROTEIN TC4; GTPASE, CHAIN: A, B; NUCLEAR TRANSPORT, TRANSPORT PROTEIN	G PROTEIN RAN;
		ZINC FING CHAIN: A;	DNA NUCI REPAIR EN CHAIN: A:	EXCINUCLE, B; CHAIN: A;	EXCINUCLE/ B; CHAIN: A;	EXCINUCI	EUKARYC	FACTOR 4	YEAST INITIATION A, B;		YEAST INITIATION 4A; CHAIN: A, B;	GTP-BINDIN CHAIN: A, B;	GTP-BINDIN(CHAIN: A, B;
SEQFOL D score													113.24
PIMF score		0.11	0.18	 0.46	0.39	0.24	0.55		-0.14		0.43	1.00	
Verify score		-0.09	0.13	 0.05	-0.11	-0.27	0.23		0.09		90.0	0.35	
Psi Blast		1.6e-34	1.6e-13	1.6e-13	1.4e-07	6.4e-17	9.6e-39	· · · · · · · · · · · · · · · · · · ·	4.8e-43		3.2e-91	7.5e-64	7.5e-64
END		490	630	 630	662	658	029		321		670	211	217
STAR T AA		344	470	470	538	457	208		105		313	14	15
CHAI N ID		¥	¥	Ą	4	A	∢		¥		м	¥	4
PDB ID		2gli	1040	 1d2m	1d2m	1d9x	ifik		1 fuu		1fuu	1byu	1byu
SEQ ID NO:		1860	1861	 1861	1861	1981	1861		1861		1861	1862	1862

Coumpound PDB annotation	GTP-BINDING PROTEIN RAN; TRANSPORT PROTEIN TC4; GTPASE, NUCLEAR TRANSPORT, TRANSPORT PROTEIN	GTP-BINDING PROTEIN RAN; TRANSPORT PROTEIN TC4; GTPASE, NUCLEAR TRANSPORT, TRANSPORT PROTEIN TRANSPORT PROTEIN	RAS-RELATED PROTEIN RAP-SIGNALING PROTEIN GTP-BINDING IA; CHAIN: A; PROTO-PROTEIN PROTEIN GOMPLEX, BFFECTORS SERINE/THREONINE PROTEIN STANDASE CHAIN: R.	RAS-RELATED PROTEIN RAP-SIGNALING PROTEIN GTP-BINDING ON KOHAN: A; PROTEIN GTP-BINDING PROTEIN; PROTEIN GTP-BINDING PROTEIN GOMPLEX, BFFECTORS SERINETHREONINE PROTEIN KINASE CHAN: B:	TRANSFORMING PROTEIN P21/H-RAS-1; CHAIN: A; CRYSTALLOGRAPHY, 2 SIGNALING PROTEIN	TRANSFORMING PROTEIN P21/H-RAS-1; CHAIN: A; CRYSTALLOGRAPHY, 2 SIGNALING PROTEIN	PROTEIN RHOA(0-181); CHAIN: PROTEIN COMPLEX, A: PKN: CHAIN: B: ANTIPARALLEL COILED-COIL	AIN: A;	ING PROTEIN YPT51;
SEQFOL D score	GTP-F	109.68 GTP-I	RAS-F 1A; CI ONKC SERIN KINA	102.67 RAS-F 1A; CI ONKC SERIN KINA!	TRAN P21/H	98.76 TRAN P21/H	95.76 HIS-T. PROTI	RAB6	GTP-BIND
PMF Score	1.00	_	00:1	-	1.00	6	δ.	1.00	1.00
Verify score	0.44		0.51		0.65			0.56	89.0
Psi Blast	1.3e-65	I.3e-65	8e-65	8e-65	6.4e-64	6.4e-54	3.2e-58	3.2e-62	9.6e-60
END	211	215	188	181	182	182	182	179	179
STAR T AA	6	6	16	17	17	17	19	18	18
CHAI N ID	æ	В	Æ	4	¥	A	A	¥	¥
EDB CI	lbyu	1byu	Icly	lcly	lotq ,	lotq /	lexz	1450	lek0 /
SEQ NO:	1862	1862	1862	1862	1862	1862	1862	1862	1862

S a S	P.D.B.	CHAI N ID	STAR T AA	END	Psi Blast	Verify score	PMF score	SEQFOL D score	Coumpound	PDB annotation
\vdash										HYDROLASE
1862 11	1ibr /	A A		281	3e-60			113.50	RAN; CHAIN: A, C; IMPORTIN BETA SHRINIT CHAIN: B. D.	SMALL GTPASE KARYOPHERIN
-	-								, , , , , , , , , , , , , , , , , , ,	NUCLEAR TRANSPORT RECEPTOR
1862 11	libr /	∢.	81	186	3e-60	08.0	1.00		RAN; CHAIN: A, C; IMPORTIN	SMALL GTPASE KARYOPHERIN
									BETA SUBUNIT; CHAIN: B, D;	BETA, P95 SMALL GTPASE, NUCLEAR TRANSPORT RECEPTOR
1862 11	1kao		17	182	9.6e-59			98.96	RAP2A; CHAIN; NULL;	GTP-BINDING PROTEIN GTP.
										BINDING PROTEIN, SMALL G PROTEIN RAP2 GDP RAS
1862 lr	lmp (၁	15	198	1.4e-60			114.45	RAN; CHAIN: A, C; NUCLEAR	COMPLEX (SMALL
									PORE COMPLEX PROTEIN	GTPASE/NUCLEAR PROTEIN)
		******						•	101 320, CIETTO, E. E.	GTPASE/NUCLEAR PROTEIN)
		-						_		SMALL GTPASE, 2 NUCLEAR
十	\dagger	,	1	;	\(\),					TRANSPORT
1802	du.		9	193	1.4e-60	0.45	8		RAN; CHAIN: A, C; NUCLEAR	COMPLEX (SMALL
-,-,-						٠			PORE COMPLEX PROTEIN	GIPASE/NUCLEAR PROTEIN)
										GTPASE/NUCLEAR PROTEIN).
										SMALL GTPASE, 2 NUCLEAR
╁	1		,							TRANSPORT
1802	TX4	<u></u>	<u>.</u>	180	4.8e-55			87.88	P50-RHOGAP; CHAIN: A;	COMPLEX(GTPASE
									TRANSFORMING PROTEIN	ACTIVATIN/PROTO-ONCOGENE)
									KHOA; CHAIN: B;	GIPASE-ACTIVATING PROTEIN
										KHOGAP; COMPLEX (GTPASE
	•	,		•				e e e e e e e e e e e e e e e e e e e		ACTIVATION/PROSE SACOGENE),
1862 12	1zbd	•	12	187	4 80-69			120.15	D A D 3 A : CHA TAI. A :	GTPASE, 2 TRANSITION STATE, GAP
		•	!	;	3			7.7.7.	PADDINI DI 24. CITADE D.	COINFLEA (GIF-
	_								MABERIETIN-3A, CHAIN: D,	BINDENGEFFECTOR) RAS-KELATED
		-							,	PROTEIN KAB3A; COMPLEX (GTP- RINDING/FEFECTOR) G PROTEIN
			-							EFFECTOR, RABCDR 2 SYNAPTIC
\dashv										EXOCYTOSIS, RAB PROTEIN,

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PDB aunotation	RAB3A, RABPHILIN	COMPLEX (GTP- BINDING/EFFECTOR) RAS-RELATED	PROTEIN RAB3A; COMPLEX (GTP-	BINDING/EFFECTOR), G PROTEIN,	EFFECTOR, RABCDR, 2 SYNAPTIC	EXOCYTOSIS, RAB PROTEIN,	NADJA, NADFRILLIN	HYDROLASE G PROTEIN, VESICULAR TRAFFICKING, GTP	HYDROLYSIS, RAB 2 PROTEIN,	NEUROTRANSMITTER RELEASE,	HYDROLASE	HYDROLASE G PROTEIN,	VESICULAR TRAFFICKING, GTP	HYDROLYSIS, RAB 2 PROTEIN,	NEUROTRANSMITTER RELEASE, HYDROLASE	COMPLEX (NUCLEAR PROTEIN(DAY) COMPLEY	OFFICE TATE OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF	(NUCLEAR FRO LEIN/RNA), KNA, SNRNP, RIBONUCLEOPROTEIN	RNA-BINDING PROTEIN/RNA TRA	PRE-MRNA; SPLICING	REGULATION, RNP DOMAIN, RNA	COMPLEX	GENE REGULATION/RNA POLY(A)	BINDING PROTEIN 1, PABP 1; RRM,	PROTEIN-RNA COMPLEX, GENE	REGULATION/RNA			GENE REGULATION/RNA POLY(A)
Coumpound		RAB-3A; CHAIN: A; RABPHILIN-3A; CHAIN: B;		<u> </u>				RAB3A; CHAIN: A;				KAB3A; CHAIN: A;		-		U2 RNA HAIRPIN IV; CHAIN: Q,	CHANGED D.	CRAIN; B, D;	SXL-LETHAL PROTEIN; CHAIN:	A, B; RNA (5'-	R(P*GP*UP*UP*UP*UP*UP*	UP*UP*UP*UP*U)- CHAIN: P, Q;	POLYDENYLATE BINDING	PROTEIN 1; CHAIN: A, B, C, D,	E, F, G, H; RNA (5'-	R(*AP*AP*AP*AP*AP*AP*	AP*AP*AP*A)-3'); CHAIN: M, N,	O, P, Q, R, S, T;	POLYDENYLATE BINDING
SEQFOL D score			7.3 7.5.						:		1000	145.01			•														
PMF score		8.						<u>8</u>	٠ ٠ .	-						0.52			0.43				0.57		_				0.43
Verify score		0.65					3	0.78		-						0.40			0.08				0.47						0.54
Psi Blast		4.8e-69						0/-as			70	07-20				7.5e-07			3e-07	, , , ,			7.5e-07						7.5e-07
END		185					5	787			100	701				202			207				205						199
STAR T AA		7					2	5			1.2	C.				135			138				138						136
CHAI N ID		∢						⊄			<	ς.				m m			Ą				∢						Ŀ.,
PDB ID		pqzI		-			3201	STAD STAD			2.mg/k) 		•		la9n	_		lb7f				lcvj					1	lcvi
SEQ NO:		1862					1062	7001			1863	7001				1864			1864			,	1864						1864

	T-11-11-11-11-11-11-11-11-11-11-11-11-11			l · · · · · · · · · · · · · · · · · · ·			, , , , , , , , , , , , , , , , , , , ,
PDB annotation	BINDING PROTEIN 1, PABP 1; RRM, PROTEIN-RNA COMPLEX, GENE REGULATION/RNA	STRUCTURAL PROTEIN PROTEIN C23; RNP, RBD, RRM, RNA BINDING DOMAIN, NUCLEOLUS	D D	RIBONUCLEOPROTEIN PTB. PTB. C198, HETEROGENEOUS NUCLEAR POLYPYRIMIDINE TRACT BINDING PROTEIN, RNP, RNA, SPICING, 2 TRANSLATION	NUCLEAR PROTEIN UI SNRNP A PROTEIN; RNA BINDING DOMAIN, NUCLEAR PROTEIN	COMPLEX (RIBONUCLEOPROTEIN/DNA) HNRNP A1, UP1; COMPLEX (RIBONUCLEOPROTEIN/DNA), HETEROGENEOUS NUCLEAR 2 RIBONUCLEOPROTEIN A1	RNA BINDING DOMAIN RNA BINDING DOMAIN, RBD, RNA RECOGNITION MOTIF, RRM, 2
Coumpound	PROTEIN 1; CHAIN: A, B, C, D, E, F, G, H; RNA (5'-R(*AP*AP*AP*AP*AP*AP*AP*AP*AP*AP*AP*AP*AP*	NUCLEOLIN RBD1; CHAIN: A;	RIBONUCLEOPROTEIN PROTEIN FROM UI SMALL NUCLEAR RIBONUCLEOPROTEIN (SNRNP UI) INRC 3 (N-TERMINAL FRAGMENT, RESIDUES 1 - 95) MUTANT WITH GLN 85 INRC 4 REPLACED BY CYS (Q8SC) INRC 5	POLYPYRIMIDINE TRACT- BINDING PROTEIN; CHAIN: A;	UI SMALL NUCLEAR RIBONUCLEOPROTEIN A; CHAIN: NULL;	HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN A1; CHAIN: A; 12-NUCLEOTIDE SINGLE-STRANDED TELOMETRIC DNA; CHAIN: B;	SEX-LETHAL; CHAIN: A, B, C;
SEQFOL D score					1 - 1 - 1 - 1 - 1 - 1 - 1 - 1 - 1 - 1 -		
PMF score		0.21	66:0	0.15	0.43	0.95	0.48
Verify score		0.48	0.13	0.20	0.05	0.32	0.38
Psi Blast		£6-07	1e-08	66-07	6e-07	7.5e-07	3e-07
END AA		961	561	196	195	196	207
STAR T AA		136	135	88	136	138	138
CHAI N ID		¥	⊕ ¤	¥		¥	A
PDB ID		1f)	lare	19m9	2u1a	Zup1	3sx[
SEQ HO NO NO		1864	1864	1864	1864	1864	1864

PDB annotation	SPLICING INHIBITOR, TRANSLATIONAL INHIBITOR, SEX 3 DETERMINATION, X CHROMOSOME DOSAGE COMPENSATION		COMPLEX (TRANSCRIPTION	FACTORDNA) COMPLEX (TRANSCRIPTION FACTOR/DNA), TRANSCRIPTION FACTOR, 2 DNA- BINDING PROTEIN	COMPLEX (TRANSCRIPTION FACTOR/DNA) COMPLEX (TRANSCRIPTION FACTOR/DNA), TRANSCRIPTION FACTOR, 2 DNA- BINDING PROTEIN	COMPLEX (INHIBITOR/NUCLEASE) COMPLEX (INHIBITOR/NUCLEASE), COMPLEX (RI-ANG), HYDROLASE 2 MOLECULAR RECOGNITION, EPITOPE MAPPING, LEUCINE-RICH 3 REPEATS	COMPLEX (INHIBITOR/NUCLEASE) COMPLEX (INHIBITOR/NUCLEASE), COMPLEX (RI-ANG), HYDROLASE 2 MOLECULAR RECOGNITION, EPITOPE MAPPING 1 FIIGINF-RICH
Coumpound		LIGASE(SYNTHETASE) SERYL- TRNA SYNTHETASE (E.C.6.1.1.11) (SERINE-TRNA LIGASE) 1SES 3 COMPLEXED WITH SERYL-HYDROXAMATE- AMP 1SES 4	T PROTEIN; CHAIN: A, B; DNA;	CHAIN: C, D;	T PROTEIN; CHAIN: A, B; DNA; CHAIN: C, D;	RIBONUCLEASE INHIBITOR; CHAIN: A, D; ANGIOGENIN; CHAIN: B, E;	RIBONUCLEASE INHIBITOR; CHAIN: A, D; ANGIOGENIN; CHAIN: B, E;
SEQFOL D score					·	·	
PMF score		0.01	09.0		0.47	0.43	0.50
Verify score		-0.21	-0.88		-0.90	0:30	0.15
Psi Blast		3.2e-05	1.6e-21		1.26-37	8e-08	1.4e-08
END		542	94		96	350	338
STAR T AA		439	I			183	209
CHAI N ID	•	∢	A		4	Ą	∢
PDB ID		1 ses	1xbr		1xbr	Ia4y	1a4y
SEQ D NO:		1865	1867	_	1867	1870	1870

1a4y A 209 373 3e-06 0.14 0.25 1d0b A 196 333 8e-07 0.40 0.12 1d0b A 196 333 8e-07 0.40 0.12 1f01 A 193 306 1.1e-06 0.03 0.03 1f01 B 193 306 1.1e-06 -0.01 0.00 1fqv A 128 349 1.1e-46 0.45 0.51 1fs2 A 128 349 4.8e-36 0.22 0.72	SEQ PDB CHAI ID ID NID NO:	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Coumpound	PDB annotation
A 209 373 3e-06 0.14 0.25 A 196 333 8e-07 0.40 0.12 A 222 354 0.00096 -0.10 0.25 A 193 306 1.1e-06 0.03 0.03 B 193 306 1.1e-46 0.45 0.51 A 128 349 4.8e-36 0.22 0.72									3 REPEATS
A 196 333 8e-07 0.40 0.12 A 222 354 0.00096 -0.10 0.25 A 193 306 1.1e-06 0.03 0.03 B 193 306 1.1e-06 0.03 0.03 A 128 349 1.1e-46 0.45 0.51 A 128 349 4.8e-36 0.22 0.72		209	373	3e-06	0.14	0.25		RIBONUCLEASE INHIBITOR; CHAIN: A, D; ANGIOGENIN;	COMPLEX (INHIBITOR/NUCLEASE),
1d0b A 196 333 8e-07 0.40 0.12 1d0b A 222 354 0.00096 -0.10 0.25 1fol A 193 306 1.1e-06 -0.01 0.03 1fol B 193 306 1.1e-06 -0.01 0.00 1fqv A 128 349 1.1e-46 0.45 0.51 1fs2 A 128 349 4.8e-36 0.22 0.72								CHAIN: B, E;	COMPLEX (RI-ANG), HYDROLASE 2
1d0b A 196 333 8e-07 0.40 0.12 1d0b A 222 354 0.00096 -0.10 0.25 1fo1 A 193 306 1.1e-06 0.03 0.03 1fo1 B 193 306 1.1e-06 -0.01 0.00 1fqv A 128 349 1.1e-46 0.45 0.51 1fs2 A 128 349 4.8e-36 0.22 0.72						-			MOLECULAR RECOGNITION, EPITOPE MAPPING, LEUCINE-RICH
140b A 222 354 0.00096 -0.10 0.25 1fol A 193 306 1.1e-06 0.03 0.03 1fol B 193 306 1.1e-06 -0.01 0.00 1fqv A 128 349 1.1e-46 0.45 0.51 1fs2 A 128 349 4.8e-36 0.22 0.72	140b	961	333	8e-07	0.40	0.12		INTERNALIN B; CHAIN: A;	STEPEALS CELL ADHESION LEUCINE RICH
1d0b A 222 354 0.00096 -0.10 0.25 1fo1 A 193 306 1.1e-06 0.03 0.03 1fo1 B 193 306 1.1e-06 -0.01 0.00 1fqv A 128 349 1.1e-46 0.45 0.51 1fs2 A 128 349 4.8e-36 0.22 0.72									REPEAT, CALCIUM BINDING, CELL ADHESION
1fol A 193 306 1.1e-06 0.03 0.03 1fol B 193 306 1.1e-06 -0.01 0.00 1fqv A 128 349 1.1e-46 0.45 0.51 1fs2 A 128 349 4.8e-36 0.22 0.72	140b	222	354	9600000	-0.10	0.25		INTERNALIN B; CHAIN: A;	CELL ADHESION LEUCINE RICH
1fol A 193 306 1.1e-06 0.03 0.03 1fol B 193 306 1.1e-06 -0.01 0.00 1fqv A 128 349 1.1e-46 0.45 0.51 1fs2 A 128 349 4.8e-36 0.22 0.72									REPEAT, CALCIUM BINDING, CELL ADHESION
Ifo1 B 193 306 1.1e-06 -0.01 0.00 Ifqv A 128 349 1.1e-46 0.45 0.51 Ifs2 A 128 349 4.8e-36 0.22 0.72		193	306	1.1e-06	0.03	0.03		NUCLEAR RNA EXPORT	RNA BINDING PROTEIN TAP (NFXI);
1fo1 B 193 306 1.1e-06 -0.01 0.00 1fqv A 128 349 1.1e-46 0.45 0.51 1fs2 A 128 349 4.8e-36 0.22 0.72								FACTOR 1; CHAIN: A, B;	RIBONUCLEOPROTEIN (RNP, RBD
Ifol B 193 306 1.1e-06 -0.01 0.00 Ifqv A 128 349 1.1e-46 0.45 0.51 Ifs2 A 128 349 4.8e-36 0.22 0.72									OR RRM) AND LEUCINE-RICH- REPEAT 2 (1 RR)
1fqv A 128 349 1.1e-46 0.45 0.51 1fs2 A 128 349 4.8e-36 0.22 0.72	161	193	306	1.1e-06	-0.01	0.00		NUCLEAR RNA EXPORT	RNA BINDING PROTEIN TAP (NFXI):
A 128 349 1.16-46 0.45 0.51 A 128 349 4.8e-36 0.22 0.72								FACTOR 1; CHAIN: A, B;	RIBONUCLEOPROTEIN (RNP, RBD
A 128 349 1.16-46 0.45 0.51 A 128 349 4.8e-36 0.22 0.72									OR RRM) AND LEUCINE-RICH-
A 128 349 1.1e-46 0.45 0.51 A 128 349 4.8e-36 0.22 0.72									REPEAT 2 (LRR)
A 128 349 4.8e-36 0.22 0.72		128	349	1.1e-46	0.45	0.51		SKP2; CHAIN: A, C, E, G, I, K, M,	LIGASE CYCLIN A/CDK2-
A 128 349 4.8e-36 0.22 0.72					-			O; SICP1; CHAIN: B, D, F, H, J, L,	ASSOCIATED PROTEIN P45; CYCLIN
A 128 349 4.8e-36 0.22 0.72								ž.	A/CDK2-ASSOCIATED PROTEIN P19;
A 128 349 4.8e-36 0.22 0.72						-			SKP1, SKP2, F-BOX, LRR, LEUCINE-
A 128 349 4.8e-36 0.22 0.72									RICH REPEAT, SCF, UBIQUITIN, 2
A 128 349 4.8e-36 0.72 0.72	+		9	,					E3, UBIQUITIN PROTEIN LIGASE
CHAIN: B, D;		128	349	4.8e-36	0.22	0.72		SKP2; CHAIN: A, C; SKP1;	LIGASE CYCLIN A/CDK2-
								CHAIN: B, D;	ASSOCIATED P45; CYCLIN A/CDK2-
						•			ASSOCIATED P19; SKP1, SKP2, F.
									BOX, LRRS, LEUCINE-RICH
									KEFEALS, SCF, 2 UBIQUITIN, E3,
1870 lyrg A 248 347 0.00064 0.09 0.27 GTPASE-ACTIVATIN	lyrg	248	347		0.09	0.27		GTPASE-ACTIVATING	TRANSCRIPTION RNA 1P: RANGAP:

PDB annotation	GTPASE-ACTIVATING PROTEIN FOR SPI1, GTPASE-ACTIVATING PROTEIN, GAP, RNAIP, RANGAP, LRR, LEUCINE- 2 RICH REPEAT PROTEIN, TWINNING, HEMIHEDRAL TWINNING, 3 MEROHEDRAL TWINNING,	ACETYLATION RNASE INHIBITOR, RIBONUCLEASE/ANGIOGENIN INHIBITOR ACETYLATION, LEUCINE-RICH REPEATS	TRANSFERASE GRK-2, BETA- ADRENERGIC RECEPTOR KINASE 1, BETA-ARK PLECKSTRIN HOMOLOGY DOMAIN, PH DOMAIN, SIGNAL TRANSDUCTION, 2 G- BETA-GAMMA BINDING DOMAIN, BETA-ADRENERGIC RECEPTOR 3 KINASE, BETA-ARK, G-PROTEIN COUPLED RECEPTOR KINASE (GRK- 2)	SIGNAL TRANSDUCTION PROTEIN	CYTOSKELETON		MEMBRANE PROTEIN CRYSTAL STRUCTURE, MEMBRANE, FERM DOMAIN, TAIL ISPAFIEN
Coumpound	PROTEIN RNA1_SCHPO; CHAIN: A, B;	RIBONUCLEASE INHIBITOR; CHAIN: NULL;	G-PROTEIN COUPLED RECEPTOR KINASE 2; CHAIN: NULL;	BETA-SPECTRIN; 1BTN 4 CHAIN: NULL; 1BTN 5	BETA-SPECTRIN; IDRO 6 CHAIN: NULL; IDRO 7	SIGNAL TRANSDUCTION PROTEIN DYNAMIN (PLECKSTRIN HOMOLOGY DOMAIN) (DYNPH) 1DYN 3	MOESIN; CHAIN: A, B; MOESIN; CHAIN: C, D;
SEQFOL D score			·				
PMF score		0.71	-0.03	96.0	0.21	0.11	0.53
Verify score		-0.03	80.0	0.19	0.22	0.13	0.05
Psi Blast		3.2e-09	4.8e-10	8e-12	1.5e-05	4.8e-10	1.6e-58
END AA		338	291	271	264	271	464
STAR T AA		209	168	172	182	186	149
CHAI N ID				·	· · · · · · · · · · · · · · · · · · ·	Ą	Ą
PDB ID		2bnh	1 bak	1btn	Idro	1dyn	lefi
SEQ NO:		1870	1871	1871	1871	1871	1871

PDB annotation	SIGNALING PROTEIN DAPPI, PHISH, BAM32; PLECKSTRIN, 3-PHOSPHOINOSITIDES, INOSITOL TETRAKISPHOSPHATE 2 SIGNAL TRANSDUCTION PROTEIN, ADAPTOR PROTEIN	SIGNALING PROTEIN DAPP1, PHISH, BAM32; PLECKSTRIN, 3-PHOSPHOINOSITIDES, INOSITOL TETRAKISPHOSPHATE 2 SIGNAL TRANSDUCTION PROTEIN, ADAPTOR PROTEIN	SIGNALING PROTEIN ARF! GUANINE NUCLEOTIDE EXCHANGE FACTOR AND PH DOMAIN	CELL ADHESION 3 SUBDOMAINS, CYTOSKELETON, CELL ADHESION	D	OXIDOREDUCTASE IPMDH, IMDH; OXIDOREDUCTASE, DECARBOXYLATING DEHYDROGENASE, LEUCINE 2 BIOSYNTHESIS	OXIDOREDUCTASE IPMDH, IMDH; OXIDOREDUCTASE,
Coumpound	DUAL ADAPTOR OF PHOSPHOTYROSINE AND 3- CHAIN: A;	DUAL ADAPTOR OF PHOSPHOTYROSINE AND 3- CHAIN: A;	GRP1; CHAIN: A;	RADIXIN; CHAIN: A;	PHOSPHORYLATION PLECKSTRIN (A-TERMINAL PLECKSTRIN HOMOLOGY DOMAIN) MUTANT 1PLS 3 WITH LEU GLU (HIS)6 ADDED TO THE C TERMINUS 1PLS 4 (INS(G105-LEHFHFHH)) (NMR, 25 STRUCTURES) 1PLS 5	3-ISOPROPYLMALATE DEHYDROGENASE; CHAIN: A, B;	3-ISOPROPYLMALATE DEHYDROGENASE; CHAIN: A,
SEQFOL D score						69.11	
PMF	0.80	0.69	0.65	0.01	0.09		0.54
Verify	0.31	0.14	0.49	-0.01	0.14		0.03
Psi Blast	3.2e-17	3.2e-17	4.8e-18	3.2e-58	1.4e-14	0	0
END	269	269	272	464	285	390	387
STAR T AA	170	170	172	134	169	10	∞
CHAI N ID	∢	∢	¥	Ą	•	¥	Ą
PDB	1fao	1fb8	Ifgy	1gc7	Ipis	1a05	1a05
SEQ B SO SO SO SO SO SO SO SO SO SO SO SO SO S	1871	1871	1871	1871	1871	1872	1872

WO 02/070539 PCT/US02/05095

PDB annotation	DECARBOXYLATING DEHYDROGENASE, LEUCINE 2 BIOSYNTHESIS	OXIDOREDUCTASE OXALOSUCCINATE	DECARBOXYLASE, IDH;	OXIDOREDUCTASE (NAD(A)-	PHOSPHORYLATION, 2 GLYOXYLATE BYPASS	OXIDOREDUCTASE	DECARBOXYLASE, IDH:	OXIDOREDUCTASE (NADÍA)	CHOH(D)), NADP,	PHOSPHORYLATION, 2	OXIDOREDUCTASE IPMDH, IMDH;	OXIDOREDUCTASE,	DEHYDROGENASE, NAD-	DEPENDANT ENZYME, 2 LEUCINE	BIOSTNI HEILC FAIRWAY	OXIDOREDUCIASE IPMDH, IMDH;	OXIDOREDUCI ASE,	DEPENDANT ENZYME 2 LETICINE	BIOSYNTHETIC PATHWAY	OXIDOREDUCTASE IPMDH, IMDH;	OXIDOREDUCTASE,	DEHYDROGENASE, LEUCINE	BIOSYNTHETIC PATHWAY, 2 NAD-	DEPENDANT ENZYME	OXIDOREDUCTASE IPMDH, IMDH; OXIDOREDUCTASE,
Coumpound	B;	ISOCITRATE DEHYDROGENASE: CHAIN:	NULL;			ISOCITRATE DEHVDPOGENASE: CHAIN:	NULL;	,		:	3-ISOPROPYLMALATE	DEHYDROGENASE; CHAIN: A,	ä	-	2000 Table Warn Care Co. C.	3-ISOPKUPYLMALAIE	DEHYDROGENASE; CHAIN: A,	Q	-33	3-ISOPROPYLMALATE	DEHYDROGENASE; CHAIN: A,	B;			3-ISOPROPYLMALATE DEHYDROGENASE; CHAIN: A,
SEQFOL D score					٠.	62.58					63.70									60.42	*******				
PMF score		0.60													;	U.41									0.65
Verify score		0.01													100	0.0 4									-0.04
Psi Blast		0				0				***************************************	0					-				0					0
END		387	****			387					382				00	387				382					389
STAR T AA		'n				7					-				-	-									-
CHAI N ID										•	Ą					T.				4					∀
PDB TD		lai2				1 ai2					1cm7					/ Hot				Icnz					lcnz
SEQ NO.		1872				1872					1872				2010	18/2				1872					1872

ound PDB annotation	DEHYDROGENASE, LEUCINE BIOSYNTHETIC PATHWAY, 2 NAD- DEPENDANT ENZYME	LATE OXIDOREDUCTASSECUESH; IIDM 7 SB; 11DM 5 CHIMERA 11DM 20 DM 6	LATE OXIDOREDUCTASE IPMDH; 1IDM 7 SE; 1IDM 5 CHIMERA 1IDM 20 DM 6	LATE OXIDOREDUCTASE IPMDH, IMDH; SE 272M6T 1XAC 10 OXIDOREDUCTASE, AIN: NULL; CHIMERA 1XAC 21	LATE OXIDOREDUCTASE IPMDH, IMDH; SE 2T2M6T 1XAC 10 OXIDOREDUCTASE, AIN: NULL; CHIMERA 1XAC 21	LATE OXIDOREDUCTASE SE; CHAIN: A, OXIDOREDUCTASE, 3- ISOPROPYLMALATE DEHYDROGENASE, LEUCINE 2 BIOSYNTHESIS, MODERATE THERMOPHILE	EATE OXIDOREDUCTASE SE; CHAIN: A, OXIDOREDUCTASE, 3- ISOPROPYLMALATE DEHYDROGENASE, LEUCINE 2 BIOSYNTHESIS, MODERATE THERMOPHILE	SSOR ANTI-ONCOGENE CELL CYCLE, A: NULL; ANTI-ONCOGENE, REPEAT, ANK REPEAT	
Coumpound	Ŕ	3-ISOPROPYLMALATE DEHYDROGENASE; 1IDM 5 CHAIN: NULL; 1IDM 6	3-ISOPROPYLMALATE DEHYDROGENASE; 11DM 5 CHAIN: NULL; 11DM 6	3-ISOPROPYLMALATE DEHYDROGENASE ZTZM6T S82R; IXAC 8 CHAIN: NULL; IXAC 9	3-ISOPROPYLMALATE DEHYDROGENASE 2T2M6T S82R; 1XAC 8 CHAIN: NULL; 1XAC 9	3-ISOPROPYLMALATE DEHYDROGENASE; CHAIN: A, B;	3-ISOPROPYLMALATE DEHYDROGENASE; CHAIN: A, B;	TUMOR SUPPRESSOR P16INK4A; CHAIN: NULL;	
SEQFOL D score		54.18	·	50.68			68.62		
PMF			0.42		0.46	0.57	A NAME OF THE OWNER OF THE OWNER OF THE OWNER OF THE OWNER OF THE OWNER OF THE OWNER OF THE OWNER OF THE OWNER	0.51	
Verify score			90.0		0.04	-0.03		0.44	,
Psi Blast		4.8e-95	4.8e-95	1.6e-96	1.6e-96 ·	0	0	1.6e-23	
END		366	387	366	387	387	3888	125	12,
STAR T AA		42	9	42	o	9	٥	10	٩
CHAI N ID		•				¥	∢		¢
PDB ID		11dm	lidm	lxac	lxac	2ayq	2ayq	1a5e].
SEQ ID NO:		1872	1872	1872	1872	1872	1872	1873	000

				,		
PDB annotation	REGULATION/DNA) GABPALPHA; GABPBETAI; COMPLEX (TRANSCRIPTION REGULATION/DNA), DNA-BINDING, 2 NUCLEAR PROTEIN, ETS DOMAIN, ANKYRIN REPEATS, TO ANSCRIPTION 2 FACTOR	COMPLEX (TRANSCRIPTION REGULATION/DNA) GABPALPHA; GABPBETAI; COMPLEX (TRANSCRIPTION REGULATION/DNA), DNA-BINDING, 2 NUCLEAR PROTEIN, ETS DOMAIN, ANKYRIN REPEATS, TRANSCRIPTION 3 FACTOR	TUMOR SUPPRESSOR TUMOR SUPPRESSOR, CDK4/6 INHIBITOR, ANKYRIN MOTIF	TUMOR SUPPRESSOR TUMOR SUPPRESSOR, CDK4/6 INHIBITOR, ANKYRIN MOTTF	COMPLEX (KINASE/ANTI- ONCOGENE) CDK6; P16INK4A, MTS1; CYCLIN DEPENDENT KINASE, CYCLIN DEPENDENT KINASE INHIBITORY 2 PROTEIN, CDK, INK4, CELL CYCLE, MULTIPLE TUMOR SUPPRESSOR, 3 MTS1, COMPLEX (KINASE/ANTI- ONCOGENE) HEADER	COMPLEX (NHIBITOR PROTEIN/KINASE) INHIBITOR PROTEIN, CYCLIN-DEPENDENT KINASE, CELL CYCLE 2 CONTROL,
Coumpound	CHAIN: A; GA BINDING PROTEIN BETA 1; CHAIN: B; DNA; CHAIN: D, E;	GA BINDING PROTEIN ALPHA; CHAIN: A; GA BINDING PROTEIN BETA 1; CHAIN: B; DNA; CHAIN: D, E;	P19INK4D CDK4/6 INHIBITOR; CHAIN: NULL;	P19INK4D CDK4/6 INHIBITOR; CHAIN: NULL;	CYCLIN-DEPENDENT KINASE 6; CHAIN: A; MULTIPLE TUMOR SUPPRESSOR; CHAIN: B;	CYCLIN-DEPENDENT KINASE 6; CHAIN: A; P19INK4D; CHAIN: B;
SEQFOL D score						
PMF score		1.00	0.11	96:0	0.62	0.15
Verify score		0.43	0.05	0.22	25.0	0.18
Psi Blast		6.4e-33	3.2e-32	1.1e-23	86-24	8e-33
END		125	157	128	125	157
STAR T AA		2	13		10	13
CHAI N ID		æ			В	æ
PDB ID		lawc	1bd8	1.bd8	1bi7	1blx
SEQ ID NO:		1873	1873	1873	1873	1873

PDB annotation	ALPHA/BETA, COMPLEX (INHIBITOR PROTEIN/KINASE)	COMPLEX (INHIBITOR PROTEIN/KINASE) INHIBITOR	PROTEIN, CYCLIN-DEPENDENT	AIPHA/BETA, COMPLEX	(INHIBITOR PROTEIN/KINASE)	HORMONE/GROWTH FACTOR P18-	P18INK4C, TUMOR, SUPPRESSOR,	CYCLIN- 2 DEPENDENT KINASE, HOBMONE GROWTH BACTOR	HORMONE/GROWTH FACTOR P18-	INK4C; CELL CYCLE INHIBITOR,	P18INK4C, TUMOR, SUPPRESSOR,	CYCLIN-2 DEPENDENT KINASE,	HORMONE/GROWTH FACTOR	SIGNALING PROTEIN HELIX-TURN-	HELIX, ANKYRIN REPEAT	CELL CYCLE INHIBITOR P18-	INK4C(INK6); CELL CYCLE	INHIBITOR, P18-INK4C(INK6),	ANKYRIN REPEAT, 2 CDK 4/6	INFIBITOR	CELL CYCLE INHIBITOR P18-	INK4C(INK6); CELL CYCLE	INHIBITOR, FIS-INK4C(INK6),	ANKYKIN KEPEAT, 2 CDK 4/6	INHIBITOR	ANK-REPEAT MYOTROPHIN, ACETYLATION, NMR. ANK-REPEAT	COMPLEX (TRANSCRIPTION	REG/ANK REPEAT) COMPLEX
Coumpound		CYCLIN-DEPENDENT KINASE 6; CHAIN: A; P19INK4D; CHAIN:	B;	•		CYCLIN-DEPENDENT KINASE 6 INHIBITOR: CHAIN: A:			CYCLIN-DEPENDENT KINASE	6 INHIBITOR; CHAIN: A;				CYCLIN-DEPENDENT KINASE	4 INHIBITOR B; CHAIN: A;	CYCLIN-DEPENDENT KINASE	6 INHIBITOR; CHAIN: A, B;	-		no rian minimum and a mino	CYCLIN-DEPENDENT KINASE	o INHIBITOR; CHAIN: A, B;				MYOTROPHIN; CHAIN: NULL	NF-KAPPA-B P65; CHAIN: A, C;	NF-KAPPA-B P50; CHAIN: B, D;
SEQFOL D score		-										en en en en									,							: : : : : : : : : : : : : : : : : : :
PMF score		96'0				0.71			0.55			•		0.49		0.60				0.74	4,7	- ·				<u>\$</u>	0.45	
Verify score		0.42				0.16			0.15					0.05		0.23				0.14	41.0	- 42.				0.21	0.02	
Psi Blast		1.6e-22				6.4e-34			4.8e-27					3.2e-24		6.4e-34				16.02	1.06-20		00.004002			1.3e-24	3.2e-40	
END AA		128				153			130					131		153				120	671					127	212	
STAR T AA		ന				10			2					9		10				,	4						4	
CHAI N ID		മ				4			A					٧		₩.				\ <	¢						ш	
PDB ID		1blx				1pn ₉			1bu9					Id9s		libb				14:	2					Imyo	1nf	
SEQ ID NO:		1873				1873			1873					1873		1873				1872	6/61					18/3	1873	

PDB annotation	(TRANSCRIPTION REGULATION/ANK REPEAT), ANKYRIN 2 REPEAT HELIX	ANTI-ONCOGENE CELL CYCLE, ANTI-ONCOGENE, REPEAT, ANK REPEAT	TUMOR SUPPRESSOR TUMOR SUPPRESSOR, CDK4/6 INHIBITOR, ANKYRIN MOTIF	TUMOR SUPPRESSOR TUMOR SUPPRESSOR, CDK4/6 INHIBITOR, ANKYRIN MOTIF	COMPLEX (KINASE/ANIT)	ONCOGENE) CDK6; P16INK4A, MTS1; CYCLIN DEPENDENT	KINASE, CYCLIN DEPENDENT	KINASE INHIBITORY 2 PROTEIN,	CDK, INK4, CELL CYCLE, MULTIPLE	TUMOR SUPPRESSOR, 3 MTS1,	ONCOGENE) HEADER	COMPLEX (KINASE/ANTI-	ONCOGENE) CDK6; P16INK4A,	MISI; CYCLIN DEPENDENT	KINASE, CI CLIN DEFENDENT	CDK TNK4 CELL CYCLE MILITIPLE	TUMOR SUPPRESSOR, 3 MTS1.	COMPLEX (KINASE/ANTI-	ONCOGENE) HEADER	COMPLEX (INHIBITOR	PROTEIN/KINASE) INHIBITOR PROTEIN, CYCLIN-DEPENDENT
Coumpound	I-KAPPA-B-ALPHA; CHAIN: E, F;	TUMOR SUPPRESSOR P16INK4A; CHAIN: NULL;	P19INK4D CDK4/6 INHIBITOR; CHAIN: NULL;	P19INK4D CDK4/6 INHIBITOR; CHAIN: NULL;	CVC! IN-DEPENDENT KINASE	6; CHAIN: A; MULTPLE TUMOR SUPPRESSOR: CHAIN:	B;					CYCLIN-DEPENDENT KINASE	6; CHAIN: A; MULTIPLE	I UMOR SUPPRESSOR; CHAIN:	i					CYCLIN-DEPENDENT KINASE	6; CHAIN: A; P19INK4D; CHAIN: B;
SEQFOL D score						-					,			V=0							
PMF score		0.81	0.31	0.01	0.68	3						0.00								0.31	
Verify score		0.03	0.03	-0.04	0 18							0.15	•							6.09	
Psi Blast	·	3.2e-16	3.2e-27	1.46-15	3.2e-17	52.4411.491						1.4e-17								3.2e-25	
END AA		120	153	120	120							153								153	
STAR T AA		10	13	2	91							25								13	
CHAI N ID					m							Д					•			щ	
PDB ID		1a5e	1bd 8	1bd8	1517		•					1bi7								Iblx	
SEQ ID NO:		1874	1874	1874	1874							1874								1874	

	PDB annotation	KINASE, CELL CYCLE 2 CONTROL, ALPHA/BETA, COMPLEX (INHIBITOR PROTEIN/KINASE)	COMPLEX (INHIBITOR PROTEIN/KINASE) INHIBITOR PROTEIN CYCLIN-DEPENDENT	ALPHA/BETA, COMPLEX (INHIBITOR PROTEIN/KINASE)	HORMONE/GROWTH FACTOR P18- INK4C; CELL CYCLE INHIBITOR, P18INK4C, TUMOR, SUPPRESSOR, CYCI IN- 2 DEPENDENT KINASE	HORMONE/GROWTH FACTOR	HORMONE/GROWTH FACTOR P18- INK4C; CELL CYCLE THEBITOR, P18INK4C, TUMOR, SUPPRESSOR, CYCLIN- 2 DEPENDENT KINASE, HORMONE/GROWTH FACTOR	HORMONE/GROWTH FACTOR P18- INK4C; CELL CYCLE INHIBITOR, P18INK4C, TUMOR, SUPPRESSOR, CYCLIN- 2 DEPENDENT KINASE, HORMONE/GROWTH FACTOR	SIGNALING PROTEIN HELIX-TURN- HELIX, ANKYRIN REPEAT	METAL BINDING PROTEIN ZINC- BINDING MODULE, ANKYRIN REPEATS, METAL BINDING PROTEIN	CELL CYCLE INHIBITOR P18- INK4C(INK6); CELL CYCLE INHIBITOR, P18-INK4C(INK6), ANKYRIN REPEAT, 2 CDK 4/6
	Coumpound		CYCLIN-DEPENDENT KINASE 6; CHAIN: A; PI9INK4D; CHAIN: B;		CYCLIN-DEPENDENT KINASE 6 INHIBITOR; CHAIN: A;		CYCLIN-DEPENDENT KINASE 6 INHIBITOR; CHAIN: A;	CYCLIN-DEPENDENT KINASE 6 INHIBITOR; CHAIN: A;	CYCLIN-DEPENDENT KINASE 4 INHIBITOR B; CHAIN: A;	PYK2-ASSOCIATED PROTEIN BETA; CHAIN: A;	CYCLIN-DEPENDENT KINASE 6 INHIBITOR; CHAIN: A, B;
projetiva, et la se se esperaj	SEQFOL D score										
	PMF		-0.09		0.23		0.11	0.05	0.33	0.69	12.0
	Verify score		80.0	•	-0.15		0.04	0.01	0.28	0.08	0.40
	Psi Blast		1.5e-14		1.3e-29		1.3e-18	6.4e-28	1.6e-17	1.5e-12	4.8e-18
	END AA		120		158		125	212	120	122	124
	STAR T AA		2		13		2	54	10	13	2
	CHAI N ID		æ	!	⋖		∢ .	4	¥	A	¥
	PDB ID		1blx		1bu9		Ibu9	1bu9	149s	1dcq	lihb
	SEQ D NO:		1874	·	1874		1874	1874	1874	1874	1874

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PDB annotation	INHIBITOR	CELL CYCLE INHIBITOR P18- INK4C(INK6); CELL CYCLE	INHIBITOR, P18-INK4C(INK6),	ANK YKIN KEFEA1, 2 CDK 4/6 INHIBITOR	ANK-REPEAT MYOTROPHIN,	ACETYLATION, NMR, ANK-REPEAT	ANK-REPEAT MYOTROPHIN,	ACETYLATION, NMR, ANK-REPEAT	COMPLEX (ANTI-	ONCOGENE/ANKYRIN REPEATS)	P53BP2; ANKYRIN REPEATS, SH3,	P53, TUMOR SUPPRESSOR,	MULTIGENE 2 FAMILY, NUCLEAR	PROTEIN, PHOSPHORYLATION,	DISEASE MUTATION, 3	POLYMORPHISM, COMPLEX (ANTI-	ONCOGENE/ANKYRIN REPEATS)	-	COMPLEX (ZINC FINGER/DNA)	COMPLEX (ZINC FINGER/DNA),	ZINC FINGER, DNA-BINDING	PROTEIN	COMPLEX (ZINC FINGER/DNA)	COMPLEX (ZINC FINGER/DNA),	ZINC FINGER, DNA-BINDING	PROTEIN	COMPLEX (ZINC FINGER/DNA)	COMPLEX (ZINC FINGER/DNA),	ZINC FINGER, DNA-BINDING	PROTEIN	COMPLEX (ZINC FINGER/DNA)	COME LES (CANOLINALINALINALINALINALINALINALINALINALINA
Coumpound		CYCLIN-DEPENDENT KINASE 6 INHIBITOR; CHAIN: A, B;			MYOTROPHIN; CHAIN: NULL		MYOTROPHIN; CHAIN: NULL		P53; CHAIN: A; 53BP2; CHAIN:	B;									QGSR ZINC FINGER PEPTIDE;	CHAIN: A; DUPLEX	OLIGONUCLEOTIDE BINDING	SITE; CHAIN: B, C;	QGSR ZINC FINGER PEPTIDE;	CHAIN: A; DUPLEX	OLIGONUCLEOTIDE BINDING	SITE; CHAIN: B, C;	QGSR ZINC FINGER PEPTIDE;	CHAIN: A; DUPLEX	OLIGONUCLEOTIDE BINDING	SITE; CHAIN: B, C;	QGSR ZINC FINGER PEPTIDE;	Citative, eye eren
SEQFOL D score															•												72.03					
PMF score		0.27			0.24		0.23		0.01										0.66				0.00								60.0	
Verify		-0.09			-0.17		0.30		-0.03							•			0.12				20.0								-0.14	
Psi Blast		3.2e-27			1.1e-21		1.1e-21		4.8e-20										9.6e-26				7.5e-29				7.5e-29		·		I.5e-39	
END		211			138		159		193										335				336				365				202	
STAR T AA		54			11		73		ල										239				243				283				395	
CHAI N ID		A				•			ഫ										₹				₩.				√.		-		∀	
PDB ID		qui l			Imyo		lmyo		lycs						-1	••			laih				laih				lalh				1217	
SEQ ID NO:		1874			1874		1874		1874										1877		•		1877	-			1877				1877	

SEQ	PDB U	CHAI	STAR T AA	END AA	Psi Blast	Verify score	PMF	SEQFOL D score	Coumpound	PDB annotation
5									OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	ZINC FINGER, DNA-BINDING PROTEIN
1877	lmey	ပ	161	263	4.8e-42	-0.16	0.06		DNA; CHAIN: A, B, D, E;	COMPLEX (ZINC FINGER/DNA) ZINC
									CONSENSUS ZINC FINGER	FINGER, PROTEIN-DNA
		<u>-</u>							PROTEIN; CHAIN: C, F, G;	INTERACTION, PROTEIN DESIGN, 2
									13	CRYSTAL STRUCTURE, COMPLEX
										(ZINC FINGER/DNA)
1877	Imey	ပ	166	307	1e-11	-0.57	0.00		DNA; CHAIN: A, B, D, E;	COMPLEX (ZINC FINGER/DNA) ZINC
								:	CONSENSUS ZINC FINGER	FINGER, PROTEIN-DNA
									PROTEIN; CHAIN: C, F, G;	INTERACTION, PROTEIN DESIGN, 2
•								-		CRYSTAL STRUCTURE, COMPLEX
										(ZINC FINGER/DNA)
1877	Imey	Ç	190	335	3e-26	-0.46	0.37		DNA; CHAIN: A, B, D, E;	COMPLEX (ZINC FINGER/DNA) ZINC
									CONSENSUS ZINC FINGER	FINGER, PROTEIN-DNA
									PROTEIN; CHAIN: C, F, G;	INTERACTION, PROTEIN DESIGN, 2
										CRYSTAL STRUCTURE, COMPLEX
										(ZINC FINGER/DNA)
1877	Imey	່ບ	217	307	8e-40	-0.24	0.07		DNA; CHAIN: A, B, D, E;	COMPLEX (ZINC FINGER/DNA) ZINC
									CONSENSUS ZINC FINGER	FINGER, PROTEIN-DNA
									PROTEIN; CHAIN: C, F, G;	INTERACTION, PROTEIN DESIGN, 2
						. * 1				CRYSTAL STRUCTURE, COMPLEX
										(ZINC FINGER/DNA)
1877	Imey	ರ	566	335	1.3e-39	0.02	0.95		DNA; CHAIN: A, B, D, E;	COMPLEX (ZINC FINGER/DNA) ZINC
		.,							CONSENSUS ZINC FINGER	FINGER, PROTEIN-DNA
									PROTEIN; CHAIN: C, F, G;	INTERACTION, PROTEIN DESIGN, 2
										CRYSTAL STRUCTURE, COMPLEX
										(ZINC FINGER/DNA)
1877	1mey	U	282	363	6.4e-50	0.29	1.00		DNA; CHAIN: A, B, D, E;	COMPLEX (ZINC FINGER/DNA) ZINC
									CONSENSUS ZINC FINGER	FINGER, PROTEIN-DNA
									PROTEIN; CHAIN: C, F, G;	INTERACTION, PROTEIN DESIGN, 2
										CRYSTAL STRUCTURE, COMPLEX
										(ZINC FINGER/DNA)
1877	Imey	ن د	282	364	8e-51			98.05	DNA; CHAIN: A, B, D, E;	COMPLEX (ZINC FINGER/DNA) ZINC
									CONSEINAGE CHINGEN	FINGER, FROIEIN-DIAR

PDB annotation	INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA	INTERACTION, PROTEIN DESIGN, 2	CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)	COMPLEX (ZINC FINGER/DNA) ZINC FINGER PROTEIN-DNA	INTERACTION, PROTEIN DESIGN, 2	CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)	COMPLEX (ZINC FINGER/DNA) ZINC	FINGER, PROTEIN-DNA	INTERACTION, PROTEIN DESIGN, 2	CRYSTAL STRUCTURE, COMPLEX	(CLINC THINDING)	COMPLEX (ZINC FINGER/DNA) ZINC	INTERACTION PROTEIN DESIGN 2	CRYSTAL STRUCTURE COMPLEX	(ZINC FINGER/DNA)	COMPLEX (ZINC FINGER/DNA) ZINC	FINGER, PROTEIN-DNA	INTERACTION, PROTEIN DESIGN, 2	CRYSTAL STRUCTURE, COMPLEX	(ZINC FINGER/DNA)	COMPLEX (ZINC FINGER/DNA) ZINC	FINGER, PROTEIN-DNA	INTERACTION, PROTEIN DESIGN, 2	CRYSTAL STRUCTURE, COMPLEX	COMPLEX (ZINC FINGER/DNA) ZINC
Coumpound	PROTEIN; CHAIN: C, F, G;	DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER	PROTEIN; CHAIN: C, F, G;		DNA; CHAIN: A, B, D, E; CONSENSIS ZINC FINGER	PROTEIN; CHAIN; C, F, G:		DNA; CHAIN: A, B, D, E;	CONSENSUS ZINC FINGER	PROTEIN; CHAIN: C, F, G;		Park, Ottable 4 m m	DINA; CHAIN: A, B, D, E;	PROTEIN: CHAIN: C. F. G.	5) (1) (1) (1) (1)		DNA; CHAIN: A, B, D, E;	CONSENSUS ZINC FINGER	PROTEIN; CHAIN: C, F, G;	All Sales and All Sales and All Sales and All Sales and All Sales and All Sales and All Sales and All Sales and All Sales and All Sales and All Sales and All Sales and All Sales and All Sales and All Sales and All Sales and All Sales and All Sales and All Sales and All Sales and All Sales and All Sales and All Sales and All Sales and All Sales and All Sales and All Sales and All Sales and All Sales and All Sales and All Sales and All Sales and All Sales and All Sales and All Sales and All Sales and All Sales and All Sales and All Sales and All Sales and All Sales and All Sales and All Sales and All Sales and All Sales and All Sales and All Sales and All Sales and All Sales and All Sales and All Sales and All Sales and All Sales and All Sales and All Sales and All Sales and All Sales and All Sales and All Sales and All Sales and All Sales and All Sales and All Sales and All Sales and All Sales and All Sales and All Sales and All Sales and All Sales and All Sales and All Sales and All Sales and All Sales and All Sales and All Sales and All Sales and All Sales and All Sales and All Sales and All Sales and All Sales and All Sales and All Sales and All Sales and All Sales and All Sales and All Sales and All Sales and All Sales and All Sales and All Sales and All Sales and All Sales and All Sales and All Sales and All Sales and All Sales and All Sales and All Sales and All Sales and All Sales and All Sales and All Sales and All Sales and All Sales and All Sales and All Sales and All Sales and All Sales and All Sales and All Sales and All Sales and All Sales and All Sales and All Sales and All Sales and All Sales and All Sales and All Sales and All Sales and All Sales and All Sales and All Sales and All Sales and All Sales and All Sales and All Sales and All Sales and All Sales and All Sales and All Sales and All Sales and All Sales and All Sales and All Sales and All Sales and All Sales and All Sales and All Sales and All Sales and All Sales and All Sales and All Sales and All Sales and All Sales and All Sales and Al		DNA; CHAIN: A, B, D, E;	CONSENSUS ZINC FINGER	PROTEIN; CHAIN; C, F, G;		DNA; CHAIN: A, B, D, E;
SEQFOL D score					-)																			
PMF score		1.00			1.00			1.00				1 00	20:1				0.82					90.1	-			1.00
Verify score		60'0			0.43			0.28				02.0	07.0		-		-0.02					0.39				0.46
Psi Blast		8e-51			3.2e-51			1.3e-50				1 80 17	- 74-20'+	-			3e-40					3.2e-48				8e-34
END AA		1981			419			447				173	5,				529					529				533
STAR T AA		310			338			366				204	+				422				[450				476
CHAI N ID		ن ن			U			၁				C	— د				ပ					ပ ပ				Ç
PDB ID		1mey			Iney			lmey				1300	tames				lmey					Imey				Imey
SEQ ID NO:		1877			1877			1877				1877					1877					1877				1877

EQ	PDB	CHAI	STAR	END	Psi Blast	Verify	PMF	SEQFOL	Coumpound	PDB annotation
A Ö	A	ND	TAA	¥		score	score	D score		
									CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX
	,	,							·	(ZINC FINGER/DNA)
1877	Imey	ڻ	187	214	1.6e-11	-0.12	0.48		DNA; CHAIN: A, B, D, E;	COMPLEX (ZINC FINGER/DNA) ZINC
									CONSENSUS ZINC FINGER	FINGER, PROTEIN-DNA
								-	PROTEIN; CHAIN: C, r, C;	INTERACTION, PROTEIN DESIGN, 2
					.,					CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1877	Imey	ŋ	236	263	6.4e-12 .	-0.05	0.52		DNA; CHAIN: A, B, D, E;	COMPLEX (ZINC FINGER/DNA) ZINC
									CONSENSUS ZINC FINGER	FINGER, PROTEIN-DNA
			-		220				PROTEIN; CHAIN: C, F, G;	INTERACTION, PROTEIN DESIGN, 2
	_									CRYSTAL STRUCTURE, COMPLEX
										(ZINC FINGER/DNA)
1877	lsp2		961	218	9.6e-07	0.02	0.09		SP1F2; CHAIN: NULL;	ZINC FINGER TRANSCRIPTION
	-									FACTOR SP1; ZINC FINGER,
										TRANSCRIPTION ACTIVATION, SP1
1877	<u>#</u>	∢	239	335	4.8e-17	0,27	0.07		TRANSCRIPTION FACTOR IIIA;	COMPLEX (TRANSCRIPTION
									CHAIN: A; 5S RNA GENE;	REGULATION/DNA) TFIIIA; 5S
					-				CHAIN: E, F;	GENE; NMR, TFIIIA, PROTEIN, DNA,
										TRANSCRIPTION FACTOR, 5S RNA 2
										GENE, DNA BINDING PROTEIN,
						•••				ZINC FINGER, COMPLEX 3
										(TRANSCRIPTION
										REGULATION/DNA)
1877	116	¥	162	316	8e-31	-0.24	0.11		TFIIIA; CHAIN: A, D; 5S	COMPLEX (TRANSCRIPTION
									RIBOSOMAL RNA GENE;	REGULATION/DIAJ COMPLEX
		•							CHAIN: B, C, E, F;	(TRANSCRIPTION
		•								REGULATION/DNA), RNA
					-			-		POLYMERASE III, 2
				-						TRANSCRIPTION INITIATION, ZINC
					-					FINGER PROTEIN
1877	3112	∢	239	99	9.6e-36	-0.06	0.75		THIIA; CHAIN: A, D; 5S	COMPLEX (TRANSCRIPTION REGIT ATTONIONA) COMPLEX
									יאנים טאטן חטאיסססמואי	ALCOUNTING COMPANY

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District Control

PDB annotation		(TRANSCRIPTION REGULATION/DNA), RNA	POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC	FINGER PROTEIN	COMPLEX (TRANSCRIPTION REGIL ATTOMONA) COMPLEY	(TRANSCRIPTION	REGULATION/DNA), RNA	POLYMERASE III, 2	I KANSCKIP I TON I NI I TATION, ZINC FINGER PROTEIN	COMPLEX (TRANSCRIPTION	REGULATION/DNA) COMPLEX		REGULATION/DNA), RNA	POL IMEKANE III, 2	TRANSCRIPTION INITIATION, ZINC	FINGER PROTEIN	COMPLEX (TRANSCRIPTION	REGULATION/DNA) COMPLEX	(TRANSCRIPTION	REGULATION/DNA), RNA	POLYMERASE III, 2	TRANSCRIPTION INITIATION, ZINC	FINGER FROTEIN	COMPLEX (TRANSCRIPTION	KEGULATION/DNA) COMPLEX	(TRANSCRIPTION	REGULATION/DNA), RNA	POLYMERASE III, 2	TRANSCRIPTION INITIATION, ZINC	FINGER PROTEIN	COMETERA (INAMACINE LIGH
Coumpound		CHAIN: B, C, E, F;			TFIIIA; CHAIN: A, D; 5S RIBOSOMAI, RNA GENE	CHAIN: B, C, E, F;				TFIIIA; CHAIN: A, D; 5S	RIBOSOMAL RNA GENE;	CHAIN: B, C, E, F;					TFIIIA; CHAIN: A, D; 5S	RIBOSOMAL RNA GENE;	CHAIN: B, C, E, F;				0 t	I FILIA; CHAIN: A, D; 5S	KIBOSOMAL KNA GENE;	CHAIN: B, C, E, F;	•.			VVI: CHAM: C. ANENO	111, CHAIN, C, ADENO-
SEQFOL	D score		5). 47 65 11:		107.85						• •		-								1										
PMF	Store		14 . 1144						ire ir	0.99							90.						200	C. 7.						0.37	6.5
Verify	SCD16	- *:	16.77							-0.02	;				2 .		0.12						2.0	<u>`</u>						-0.30	2.32
Psi Blast					7.5e-68	•				8e-38			•				4.8e-38				=1104		70.0	96-34						1 46-26	
END	5				471					454						-	511						221	7			-			335	255
STAR	WW 1				310					311							367						205	242						165	3
CHAI					⋖			-		¥					•		⊀						1	τ.	•••				-,-·	U	,
PDB	3			7	1±6			.		11.16							<u>+</u>				~		1 +54	2						1ubd	1
SEQ	Ş Ş				1877					1877						1	1877						1077	701						1877	

SEQ FDB CHAI STAR END Fis Blast Verify PMT SEQPOL Coungoound PDB annotation					, <u> </u>	
PDB CHAI STAR END Psi Blast Verify PMF SEQFOL	PDB annotation	REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)	COMPLEX (TRARSCERTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION,
PDB CHAI STAR END Fis Blast Verify PMF	Coumpound	ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	YYI; CHAIN: C; ADENO- ASSOCIATED VIRUS PS INITIATOR ELEMENT DNA; CHAIN: A, B;	YYI; CHAIN: C; ADENO- ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	YYI; CHAIN: C; ADENO- ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	YYI; CHAIN: C; ADENO- ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA;
PDB CHAI STAR END Fsi Blast Verify	SEQFOL D score					
PDB CHAI STAR END Psi Blast Iubd C 243 363 7.5e-40 Iubd C 246 363 6.4e-33 Iubd C 287 391 3e-50 0 Iubd C 287 318 419 3.2e-35 -	PMF		0.98	0.86	1.00	0.95
PDB CHAI STAR END Psi	Verify score		-0.00	-0.09	0.00	-0.13
PDB CHAI STAR	Psi Blast		7.5e-40	6.4e-33	3e-50	3.2e-35
Inbd C Iubd C Iu	END		363	363	391	419
PDB Iubd Iubd Iubd	STAR T AA		243	246	287	318
	CHAI N ID		.	ပ	υ υ	ပ
SEQ DO NO: 1877 1877	PDB ID		Iubd	lubd	lubd	lubd
	SEQ NO:		1877	1877	1877	1877

PDB annotation		INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION	COMPLEX (TRANSCRIPTION COMPLEX (TRANSCRIPTION TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY 1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGIL ATTOM/DNA)	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN
Coumpound		CHAIN: A, B, FID FID FID RE	YY1; CHAIN: C; ADENO-CCASSOCIATED VIRUS P5 INITIATOR ELEMENT DINA; TR CHAIN: A, B; FIN FIN FIN FIN FIN FIN FIN FIN FIN FIN	YYI; CHAIN: C; ADENO-CC ASSOCIATED VIRUS PS REINITIATOR ELEMENT DNA; TR CHAIN: A, B; FIN	YYI; CHAIN: C; ADENO-CC ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; TR CHAIN: A, B; FIN FIN RE	YYI; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; IRCHAIN: A, B; INITIATOR ELEMENT DNA; INITIATOR EL
SEQFOL	D score		86.32			
PMF	score			66:0	0.95	0.99
Verify	score			0.26	0.03	0.10
Psi Blast			3e-48	1.16-47	4.8e-32	3e-48
END	AA		8 8 8	474 4	473	501
STAR	TAA		340	364	374	392
CHAI	9		ပ	U	S	U
PDB	A	***************************************	lubd	Jubd	lubd	pqnl
SEQ	Αÿ		1877	1877	1877	1877

PDB annotation	RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN	RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION,	INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX	(Irenscription REGULATION/DNA)	TRANSCRIPTION REGULATION TRANSCRIPTION REGULATION, ADR1, ZINC FINGER, NMR	TRANSCRIPTION REGULATION TRANSCRIPTION REGULATION, ADRI. ZINC FINGER, NMR	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI:	GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI;	GLI, ZINC FINGER, COMPLEA (DINA: BINDING PROTEIN/DNA)	COMPLEX (DNA-BINDING
Coumpound		YYI; CHAIN: C; ADENO- ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;		YYI; CHAIN: C; ADENO- ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA;	CHAIN: A, B;		ADRI; CHAIN: NULL;	ADR1; CHAIN: NULL;	ZINC FINGER PROTEIN GLII; CHAIN: A; DNA; CHAIN: C. D;		ZINC FINGER PROTEIN GLII; CHAIN: A; DNA; CHAIN: C, D;		ZINC FINGER PROTEIN GLII;
SEQFOL D score						-					ž t		93.76
PMF score		1.00		1.00			0.41	0.63	0.80		0.41		
Verify score		0.12	i	-0.08			-0.48	-0.23	0.15	`%. _.	0.19		
Psi Blast		1.56-48	-	8e-34			1.3e-14	1.6e-12	1.5e-46		3.2e-33		1.5e-66
END		530		529			216	309	365		390		421
STAR T AA		420		430			162	239	190		246		282
CHAI N ID		O		J					¥		∢		A
PDB		pqn1		lubd	· · · · · · · · · · · · · · · · · · ·		2adr	2adr	2gli		2gli		2gli
SEQ ID NO:	****	1877		1877	•		1877	1877	1877	*********** * *	1877		1877

nd PDB annotation	AIN: C, D; PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)	AIN: C, D; PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING) PROTEIN/DNA)	AIN: C, D; PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING) BINDING PROTEIN/DNA)		DE. HEXAMERIZATION DOMAIN PROTEIN; HEXAMERIZATION DOMAIN, ATPASE, TRANSPORT				EIN HSLU; CHAPERONE AAA-ATPASE, CLPY, ATP-DEPENDEN BRACKED VSIS	EIN HSLU; CHAPERONE AAA-ATPASE, CLPY, ATP-DEPENDENT PROTEOLYSIS	HOSPHATE TRANSFERASE CK; NUCLEOTIDE MONOPHOSPHATE KINASE,
Coumpound	CHAIN: A; DNA; CHAIN: C, D;	ZINC FINGER PROTEIN GLII; CHAIN: A; DNA; CHAIN: C, D;	ZINC FINGER PROTEIN GLII; CHAIN: A; DNA; CHAIN: C, D;		N-ETHYLMALEIMIDE- SENSITIVE FUSION PROTEIN; CHAIN: A:	N-ETHYLMALEIMIDE- SENSITIVE FUSION PROTEIN; CHAIN: A:	HEAT SHOCK PROTEIN HSLV; CHAIN: A, B, C, D; HEAT SHOCK PROTEIN HSLU; CHAIN: E. F:	CELL DIVISION CONTROL PROTEIN 6; CHAIN: A, B;	HEAT SHOCK PROTEIN HSLU; CHAIN: A;	HEAT SHOCK PROTEIN HSLU; CHAIN: A;	CYTIDINE MONOPHOSPHATE KINASE; CHAIN: A;
SEQFOL D score					65.03						
PMF score		0.27	0.93			9.0	0.10	0.28	0.57	0.23	0.15
Verify score		-0.16	-0.16	_		0.35	-0.74	0.22	0.00	0.16	-0.51
Psi Blast		1.5e-66	6e-53		3.2e-15	3.2e-15	3.2e-13	1.5e-15	1.6e-16	4.5e-34	0.0045
END		503	533		424	349	270	405	360	442	245
STAR T AA		310	395		169	196	691	184	691	183	218
CHAI N ID		A	V		¥	4	ш	4	¥	∢	¥.
PDB ID		2gli	2gli		1d2n	1d2n	1e94	1fm	1g41	1g41	2cmk
SEQ NO D		1877	1877		1878	1878	1878	1878	1878	1878	1878

	ion	TOSOLIC SFERASE, OF	OSOLIC FERASE, ATE,			S. S, E, SING		ZIED.
	PDB annotation	AMINOTRANSFERASE CYTOSOLIC ASPARTATE AMINOTRANSFERASE, PIG, IN THE 2 PRESENCE OF LIGAND 2-METHYLASPARTATE, AMINOTRANSFERASE	AMINOTRANSFERASE CYTOSOLIC ASPARTATE AMINOTRANSFERASE, PIG, IN THE 2 PRESENCE OF LIGAND 2-METHYLASPARTATE, AMINOTRANSFERASE		9	TRYPTOPHAN BIOSYNTHESIS TRYPTOPHAN INDOLE-LYASE; TRYPTOPHAN BIOSYNTHESIS, TRYPTOPHAN INDOLE-LYASE, PYRIDOXAL 2 5-PHOSPHATE, MONOVALENT CATION BINDING SITE	LYASE ACC SYNTHASE, S- ADENOSYL-L-METHIONINE ETHYLENE BIOSYNTHESIS	RIFAMYCIN BIOSYNTHESIS (RIFD
	Соитроива	ASPARTATE AMINOTRANSFERASE; CHAIN: A, B;	ASPARTATE AMINOTRANSFERASE; CHAIN: A, B;	TRANSFERASE(AMINOTRANSF ERASE) ASPARTATE AMINOTRANSFERASE (E.C.2.6.1.1) COMPLEXED WITH 1ARS 3 PYRIDOXAL-5'- PHOSPHATE 1ARS 4	TRANSFERASE(AMINOTRANSF ERASE) ASPARTATE AMINOTRANSFERASE (E.C.2.6.1.1) COMPLEXED WITH 1ARS 3 PYRIDOXAL-5'- PHOSPHATE 1ARS 4	TRYPTOPHANASE; CHAIN: A, B, C, D;	I-AMINOCYCLOPROPANE-I- CARBOXYLATE SYNTHASE; CHAIN: A, B;	3-AMINO-5-
lynesia jakin on saida. Madila (jakin on mada).	SEQFOL D score	77.13	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1		76.94	71.45		
Appelo (Mario) (Mario) Application (Mario) Application (Mario)	PMF score	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	0.88	0.51	·		1.00	0.33
janan jaki dan keperanja. Manusinggali dan peranja	Verify score	इ.स. १	0.08	61. 0		-	0.44	0.08
Topic Congression Congression	Psi Blast	1.6e-58	1.6e-58	1.6e-54	1.6e-64	4.8e-13	0	1.6e-10
	END	499	517	457	508	523	515	304
i v	STAR T AA	54	8	8	95	89	80	181
	CHAI N ID	4	A			∢	¥	A
Terror	PDB ID	lajs	lajs	lars	lars	1ax4	168g	169h
	SEQ NO:	1882	1882	1882	18882	28 82 82	1882	1882

PDB annotation	GENE) AHBA SYNTHASE; RIFAMYCIN BIOSYNTHESIS (RIFD GENE)	AMINOTRANSFERASE AMINOTRANSFERASE, PYRIDOXAL ENZYME	AMINOTRANSFERASE AMINOTRANSFERASE, PYRIDOXAL ENZYME	TRANSFERASE TAT; TYROSINE CATABOLISM, TRANSFERASE, AMINOTRANSFERASE, 2 PYRIDOXAL-5-PUGGGGGGTTE, FLP		TRANSFERASE TRANSFERASE, AMINOTRANSFERASE, PYRIDOXAL PHOSPHATE	LYASE CGS; LYASE, LLP- DEPENDENT ENZYMES, METHIONINE BIOSYNTHESIS	TRANSFERASE AMINOTRANSFERASE FOLD, LARGE PLP-BINDING DOMAIN, SMALL C- 2 TERMINAL DOMAIN, OPEN ALPHA-BETA STRUCTURE.	TRANSFERASE SHMT, SERINE METHYLASE; ALPHA PLP ASPARTATE, AMINO TRANSFERASE, (AAT)-LIKE FOLD	LYASE FES CLUSTER BIOSYNTHESIS, PYRIDOXAL 5'-
Coumpound	HYDROXYBENZOIC ACID SYNTHASE; CHAIN: A;	ASPARTATE AMINOTRANSFERASE; CHAIN: A, B;	ASPARTATE AMINOTRANSFERASE; CHAIN: A, B;	TYROSINE AMINOTRANSFERASE; CHAIN: A, B;	TYROSINE AMINOTRANSFERASE; CHAIN: A, B;	CYSTALYSN; CHAIN: A, B, C, D, E, F, G, H;	CYSTATHIONINE GAMMA- SYNTHASE; CHAIN: A, B, C, D;	MALY PROTEIN; CHAIN: A, B;	SERINE HYDROXYMETHYLTRANSFER ASE; CHAIN: A, B, C, D;	L'CYSTEINE/L-CYSTINE C-S LYASE; CHAIN: A, B;
SEQFOL D score			134.98		158.29					
PMF		1.00		1.00		1.00	0.13	1.00	1.00	0.87
Verify score		0.52		0.24	, ,	0.34	-0.10	0.35	0.42	0.17
Psi Blast		9.6e-84	9.6e-84	1.6e-67	1.6e-67	6e-52	1.6e-08	4.5e-53	4.8e-07	9.6e-13
END AA		515	514	520	520	514	302	514	415	514
STAR T AA		102	æ	99	. 26	125	441	128	182	123
CEAI N ID		∢	ď	A	Ą	¥	4	¥	A	Ą
PDB ID		w[q]	1bjw	1bw0	1bw0	lc7n	lcs1	1d2f	Idfo	lelu
SEQ ID NO:		1882	1882	1882	1882	1882	1882	1882	1882	1882

SEQ PDB CHAI STAR EVD Fel Blast Verify PMT SEQPOL Compound PDB annountion PDB announties PDB announ										
PDB CHAI STAR END Pil Blast Verify PMF SEQFOL	PDB annotation	PHOSPHATE, 2 THIOCYSTEINE, AMINOACRYLATE, ENZYME- PRODUCT COMPLEX	AMINOTRANSFERASE TRANSFERASE, AMINOTRANSFERASE	AMINOTRANSFERASE TRANSFERASE, AMINOTRANSFERASE	AMINOTRANSFERASE AROAT; AMINOTRANSFERASE	AMINOTRANSFERASE AROAT; AMINOTRANSFERASE			LYASE LYASE, PLP-DEPENDENT ENZYME, PYRIDOXAL PHOSPHATE	AMINOTRANSFERASE PHEAT, TYRAT, AROAT; AMINOTRANSFERASE, AROMATIC
PDB CHAI STAR END Psi Blast Verify PMF	Coumpound		ASPARTATE AMINOTRANSFERASE; CHAIN: A. B. C. D:	ASPARTATE AMINOTRANSFERASE; CHAIN: A. B. C. D:	AROMATIC AMINO ACID AMINOTRANSFERASE; CHAIN: A. B:	AROMATIC AMINO ACID AMINOTRANSFERASE; CHAIN: A. B:	TRANSFERASE(AMINOTRANSF ERASE) ASPARTATE AMINOTRANSFERASE (CASPAT) (E.C.2.6.1.1) 2CST 3 COMPLEXED WITH PYRIDOXAL-5'-PHOSPHATE AND MALEATE 2CST 4	TRANSFERASE(AMINOTRANSF ERASE) ASPARTATE AMINOTRANSFERASE (CASPAT) (E.C.2.6.1.1) 2CST 3 COMPLEXED WITH PYRIDOXAL-5'-PHOSPHATE AND MALRATE 2CST 4	TYROSINE PHENOL-LYASE; CHAIN: A. B:	TYROSINE AMINOTRANSFERASE; CHAIN: A, B, C, D, E, F;
PDB CHAI STAR END Psi Blast Verify Score PDB	SEQFOL D score		79.51		74.67			75.00		
PDB CHAI STAR END Psi Blast Iyaa A 76 516 4.8e-52 Iyaa A 76 516 4.8e-52 Zayi A 85 457 8e-53 Zcst A 81 517 1.6e-58 Zcst A 88 499 1.6e-58 Ztpl A 110 508 1.1e-48 0 Ztpl A 80 457 9.6e-58 Ztpl A 80 457 9.6e-58	PMF score			1.00		0.88	0.95		0.34	0.95
PDB CHAI STAR END FSI	Verify score			0.06		-0.16	-0.13		0.01	-0.17
PDB CHAI STAR ID			4.8e-52	4.8e-52	8e-53	8e-53	1.6e-58	1.6e-58	1.1e-48	9.6e-58
PDB CHAI	END		516	452	488	457	517	499	208	457
PDB	STAR T AA		76	68	62	82	81	88	011	08
	CHAI		¥	Ą	A	¥	Ą	¥	Ą	4
SEQ NO: 1882 1882 1882 1882 1882 1882 1882 188	PDB TD		lyaa	Iyaa	2ayl	2ayî	2cst	2cst	2tpl	3tat
	SEQ EQ		1882	1882	1882	1882	1882	1882	1882	1882

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PDB annotation	SUBSTRATES, PLP ENZYME	AMINOTRANSFERASE PHEAT, TYRAT, AROAT; AMINOTRANSFERASE, AROMATIC SUBSTRATES, PLP ENZYME				HYDROLASE TYROSINE PHOSPHATEASE, LAR PROTEIN	HYDROLASE DUAL SPECIFICITY PHOSPHATASE, MAP KINASE HYDROLASE	HYDROLASE DUAL SPECIFICITY PHOSPHATASE, MAP KINASE HYDROLASE	HYDROLASE VHR; HYDROLASE, PROTEIN DUAL-SPECIFICITY PHOSPHATASE	HYDROLASE VHR; HYDROLASE, PROTEIN DUAL-SPECIFICITY PHOSPHATASE		IMMUNOGLOBULIN
Coumpound		TYROSINE AMINOTRANSFERASE; CHAIN: A, B, C, D, E, F;	TRANSFERASE(AMINOTRANSF ERASE) ASPARTATE AMINOTRANSFERASE (E.C.2.6.1.1) COMPLEX WITH 7AAT 3 PYRIDOXAL-5'- PHOSPHATE AT PH 7.5.7AAT 4	TRANSFERASE(AMINOTRANSF ERASE) ASPARTATE AMINOTRANSFERASE (E.C.2.6.1.1) COMPLEX WITH 7AAT 3 PYRIDOXAL-5- PHOSPHATE AT PH 7.5 7AAT 4		LAR; CHAIN: A, B;	PYST1; CHAIN: NULL;	PYST1; CHAIN: NULL;	HUMAN VHI-RELATED DUAL- SPECIFICITY PHOSPHATASE CHADI: A. B:	HUMAN VHI-RELATED DUAL- SPECIFICITY PHOSPHATASE CHAIN: A, B;		ANTIBODY CTM01; CHAIN: L,
SEQFOL D score		91.42		78.03			68.80		139.04			
PMF score			0.43			0.18		1.00		1.00		1.00
Verify score		,	-0.10			-0.13		0.57		0.74		0:30
Psi Blast		9,6e-58	6.4e-65	6.4e-65		1.1e-58	6.4e-24	6.4e-24	7.Se-31	7.5e-31		9.6e-82
END AA		497	457	492		220	200	200	208	200		242
STAR T AA		95	73	8		3	52	55	37	50		20
CRAI N ID		¥	∀	A		В			¥	A		出
PDB ID		3tat	7aat	7aat		Har	lmkp	Imkp	lvhr	lvhr		1ae6
SEQ No:		1882	1882	1882		1883	1883	1883	1883	1883		1884

PDB annotation	IMMUNOGLOBULIN, FAB FRAGMENT, HUMANISATION	COMPLEX (VIRAL. CAPSID/IMMUNOGLOBULIN) HIV-1 CA, HIV CA, HIV P24, P24; FAB, FAB LIGHT CHAIN, FAB HEAVY CHAIN COMPLEX (VIRAL. CAPSID/IMMUNOGLOBULIN), HIV,	COMPLEX (MHC.VIRAL PEPTIDERECEPTOR) HLA A2 HEAVY CHAIN; COMPLEX (MHC/VIRAL PEPTIDE/RECEPTOR)	COMPLEX (MHC/VIRAL PEPTIDE/RECEPTOR.) HLA A2 HEAVY CHAIN; COMPLEX (MHC/VIRAL PEPTIDE/RECEPTOR.)	RECEPTOR T CELL RECEPTOR 1BEC 14	IMMUNE SYSTEM IMMUNE SYSTEM	IMMUNOGLOBULIN FAB, ANTIBODY, ANTIGEN, HIV-1, P24, CA	
Coumpound	H;	HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 CAPSID CHAIN: A, B; ANTIBODY FAB25.3 FRAGMENT; CHAIN: H, K, L, M;	HLA-A 0201; CHAIN: A; BETA-2 MICROGLOBULIN; CHAIN: B; TAX PEPTIDE; CHAIN: C; T CELL RECEPTOR ALPHA; CHAIN: D; T CELL RECEPTOR BETA; CHAIN: E;	H.A.A 0201; CHAIN: A; BETA-2 MICROGLOBULIN; CHAIN: B; TAX PEPTIDE; CHAIN: C; T CELL RECEPTOR ALPHA; CHAIN: D; T CELL RECEPTOR BETA; CHAIN: B;	14.3.D T CELL ANTIGEN RECEPTOR; 1BEC 5 CHAIN: NULL; 1BEC 6	CHIMERIC GERMLINE PRECURSOR OF OXY-COPE CHAIN: L; CHIMERIC GERMLINE PRECURSOR OF OXY-COPE CHAIN: H;	IMMUNOGLOBULIN LIGHT CHAIN; CHAIN; L; IMMUNOGLOBULIN HEAVY CHAIN; CHAIN: H;	IMMUNOGLOBULIN FAB
SEQFOL D score			301.81		273.44			
PMF score		00'1		1.00		0,99	1.00	1.00
Verify score		0.43		0.66		0.23	0.40	0.18
Psi Blast		8e-84	1.2e-81	1.2e-81	1.5e-76	1.3e-81	4.8e-81	1.1e-84
END AA		244	261	261	261	244	244	247
STAR T AA		20	21	22	21	82	ଛ	20
CHAI N ID		Ħ	田	<u></u>		ш	H	В
PDB ID		lafv	ZPq1	1 <u>b</u> d2	1bec	<u>1</u> 45i	le60] Lyd
SEQ NO:		1884	1884	1884	1884	1884	1884	1884

SEQFOL D score
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277.99

PDB annotation	REPRESSOR, ZINC-FINGER PROTEIN, X-RAY CRYSTALLOGRAPHY, 3 PROTEIN STRUCTURE, PROMYELOCYTIC LEUKEMIA, GENE REGULATION	GENE REGULATION POZ DOMAIN; PROTEIN-PROTEIN INTERACTION DOMAIN, TRANSCRIPTIONAL 2 REPRESSOR, ZINC-FINGER PROTEIN, X-RAY CRYSTALLOGRAPHY, 3 PROTEIN STRUCTURE, PROMYELOCYTIC LEUKEMIA, GENE REGULATION			RNA-BINDING PROTEIN/RNA TRA PRE-MRNA; SPLICING REGULATION, RNP DOMAIN, RNA COMPLEX	GENE REGULATION/RNA POLY(A) BINDING PROTEIN 1, PABP 1; RRM, PROTEIN-RNA COMPLEX, GENE REGULATION/RNA	GENE REGULATION/RNA POLY(A) BINDING PROTEIN 1, PABP 1; RRM, PROTEIN-RNA COMPLEX, GENE REGULATION/RNA
Coumpound		PROMYELOCYTIC LEUKEMIA ZINC FINGER PROTEIN PLZF; CHAIN: A;	OXIDOREDUCTASE(OXYGEN(A)) GALACTOSE OXIDASE (E.C.1.1.3.9) (PH 4.5) 1GOF 3	OXIDOREDUCTASE(OXYGEN(A)) GALACTOSE OXIDASE (E.C.1.1.3.9) (PH 4.5) 1GOF 3	SXL-LETHAL PROTEIN; CHAIN: A, B; RNA (5'- R(P*GP*UP*UP*UP*UP* UP*UP*UP*UP*U)- CHAIN: P, Q;	POLYDENYLATE BINDING PROTEIN 1; CHAIN: A, B, C, D, E, F, G, H; RNA (5'- R(*AP*AP*AP*AP*AP*AP* AP*AP*AP*AP; CHAIN: M, N, O, P, O, R, S, T;	POLYDENYLATE BINDING PROTEIN 1; CHAIN: A, B, C, D, E, F, G, H; RNA (5'- R(*AP*AP*AP*AP*AP*AP*
SEQFOL D score		59.44					
PMF			0.27	0.12	1.00	1.00	0.89
Verify score	·		0.31	0.36	0.53	0.41	0.41
Psi Blast		4.8e-24	1.2e-32	6.4e-12	9e-05	3e-05	3e-05
END		₹: 1	551	555	1410	1410	1410
STAR T AA		6	291	301	1342	1342	1340
CEAI N ID		4		•	Ą	4	æ
PDB ID		16uo	1gof	1gof	167f	levj	lcvj
SEQ TO NO:		1886	1886	1886	1887	1887	1887

PDB annotation	-	RNA BINDING PROTEIN RNA- BINDING DOMAIN	STRUCTURAL PROTEIN PROTEIN C23; RNP, RBD, REMARK BINDING DOMAIN, NUCLEOLUS	OUTER MEMBRANE PROTEIN OSMOPORIN; OUTER MEMBRANE PROTEIN, NON-SPECIFIC PORIN, OSMOPORIN, 2 BETA-BARREL, TRANSMEMBRANE		HYDROLASE DOUBLE BETA BARREL, BACTERIAL SERINE PROTEASE		RNA-BINDING DOMAIN RNA- BINDING DOMAIN, ALTERNATIVE SPLICING	RNA-BINDING PROTEIN SPLICING, U2 SNRNP, RBD, RNA-BINDING PROTEIN	RNA BINDING DOMAIN RNA BINDING DOMAIN, RBD, RNA RECOGNITION MOTIF, RRM, 2
Coumpound	AP*AP*AP*A}-3); CHAIN: M, N, O, P, Q, R, S, T;	HU ANTIGEN C; CHAIN: A;	NUCLEOLIN RBD2; CHAIN: A;	OMPK36; CHAIN: A, B, C;	OUTER MEMBRANE PROTEIN PHOSPHOPORIN (PHOE) IPHO 3	ALPHA-LYTIC PROTEASE; CHAIN: A;	RNA-BINDING PROTEIN SEX- LETHAL PROTEIN (C- TERMINUS, OR SECOND RNA- BINDING DOMAIN 1SXL 3 (RBD-2), RESIDUES 199 - 294 PLUS N-TERMINAL MET) 1SXL 4 (NMR, 17 STRUCTURES) 1SXL	SEX-LETHAL PROTEIN; CHAIN: NULL;	SPLICING FACTOR U2AF 65 KD SUBUNIT; CHAIN: A;	SEX-LETHAL; CHAIN: A, B, C;
SEQFOL D score										
PMF score		1.00	0.65	-0.20	-0.19	-0.19	0.54	1.00	0.99	0.55
Verify score		0.45	0.42	0.70	0.77	68.0	0.07	0.47	0.44	0.01
Psi Blast		4.5e-05	3e-05	4.5e-09	7.5e-10	4.5e-08	0.00015	0.00015	1.3e-05	ee-05
END AA		1410	1417	207	218	204	1396	1410	1410	1432
STAR T AA		1342	1331	41	11	37	1325	1339	1342	1339
CHAI N ID		4	∢	A •		₹ .			٧	∢
PDB ID		78p]	1fjc	losm	1pho	1994	lsxi	2sxl	2u2f	3sx1
SEQ NO.		1887	1887	1887	1887	1887	1887	1887	1887	1887

ı⊢. I	STAR E	END AA	Psi Blast	Verify	PMF score	SEQFOL D score	Coumpound	PDB annotation SPLICING INHIBITOR,
								TRANSLATIONAL INHIBITOR, SEX 3 DETERMINATION, X CHROMOSOME DOSAGE COMPENSATION
1303	H	1371	9e-05	0.53	1.00		SXL-LETHAL PROTEIN; CHAIN: A, B; RNA (5*- R(P*GP*UP*UP*UP*UP*UP* UP*UP*UP*UP*U>, Q;	RNA-BINDING PROTEIN/RNA TRA PRE-MRNA; SPLICING REGULATION, RNP DOMAIN, RNA COMPLEX
1303	[-	1371	3e-05	0.41	1.00		POLYDENYLATE BINDING PROTEIN 1; CHAIN: A, B, C, D, E, F, G, H; RNA (5'- R(*AP*AP*AP*AP*AP*AP* AP*AP*AP*A)-3'); CHAIN: M, N, O, P, Q, R, S, T;	GENE REGULATION/RNA POLY(A) BINDING PROTEIN I, PABP I; RRM, PROTEIN-RNA COMPLEX, GENE REGULATION/RNA
1301		1371	3e-05	0.41	0.89		POLYDENYLATE BINDING PROTEIN I; CHAIN: A, B, C, D, E, F, G, H; RNA (5'- R(*AP*AP*AP*AP*AP*AP* AP*AP*AP*AP* O, P, Q, R, S, T;	GENE REGULATION/RNA POLY(A) BINDING PROTEIN 1, PABP 1; RRM, PROTEIN-RNA COMPLEX, GENE REGULATION/RNA
1303	ļ⊷i	371	4.5e-05	0.45	1.00		HU ANTIGEN C; CHAIN: A;	RNA BINDING PROTEIN RNA- BINDING DOMAIN
1292		1378	3e-05	0.42	0,65		NUCLEOLIN RBD2; CHAIN: A;	STRUCTURAL PROTEIN PROTEIN C23; RNP, RBD, RRM, RNA BINDING DOMAIN, NUCLEOLUS
14	2	207	4.5e-09	0.70	-0.20		OMPK36; CHAIN: A, B, C;	OUTER MEMBRANE PROTEIN OSMOPORIN; OUTER MEMBRANE PROTEIN, NON-SPECIFIC PORIN, OSMOPORIN, 2 BETA-BARREL, TRANSMEMBRANE
	2		7.5e-10	0.77	-0.19		OUTER MEMBRANE PROTEIN PHOSPHOPORIN (PHOE) 1PHO 3	
37	7	204	4.5e-08	68.0	-0.19		ALPHA-LYTIC PROTEASE;	HYDROLASE DOUBLE BETA

					1	-	·	_		
	PDB annotation		BARREL, BACTERIAL SERINE PROTEASE		RNA-BINDING DOMAIN RNA- BINDING DOMAIN, ALTERNATIVE SPLICING	RNA-BINDING PROTEIN SPLICING, U2 SNRNP, RBD, RNA-BINDING PROTEIN	RNA BINDING DOMAIN RNA BINDING DOMAIN, RBD, RNA RECOGNITION MOTIF, RRM, 2 SPLICING INHIBITOR, TRANSLATIONAL INHIBITOR, SEX 3 DETERMINATION, X CHROMOSOME DOSAGE COMPENSATION		RNA-BINDING PROTEIN/RNA TRA PRE-MRNA; SPLICING REGULATION, RNP DOMAIN, RNA COMPLEX	GENE REGULATION/RNA POLY(A) BINDING PROTEIN 1, PABP 1; RRM, PROTEIN-RNA COMPLEX, GENE REGULATION/RNA
	Commbound		CHAIN: A;	RNA-BINDING PROTEIN SEX- LETHAL PROTEIN (C- TERMINUS, OR SECOND RNA- BINDING DOMAIN 15XL 3 (RBD-2), RESIDUES 199 - 294 PLUS N-TERMINAL MET) 15XL 4 (NMR, 17 STRUCTURES) 15XL 5	SEX-LETHAL PROTEIN; CHAIN: NULL;	SPLICING FACTOR U2AF 65 KD SUBUNIT; CHAIN: A;	SEX-LETHAL; CHAIN: A, B, C,		SXL-LETHAL PROTEIN; CHAIN: A, B; RNA (5'- R(P*GP*UP*UP*UP*UP* UP*UP*UP*UP*UP-CHAIN: P, Q;	POLYDENYLATE BINDING PROTEIN I; CHAIN: A, B, C, D, E, F, G, H; RNA (5'- R(*AP*AP*AP*AP*AP*AP* AP*AP*AP*A):; CHAIN: M, N, O, P, Q, R, S, T;
	SEQFOL	D score								
	PMF	score		0.54	1.00	0.99	0.55		1.00	1.00
· .	Verify	score	· (-)	0.07	0.47	0.44	0.01		0.53	0.41
	Psi Blast		٠.	0.000015	0.00015	1.3e-05	6e-05		9e-05	3e-05
	ES :	¥¥		1357	1371	1371	1393		1313	1313
	STAR	V 2 1		1286	1300	1303	1300		1245	1245
	CHAI	3				K	¥		A	Ą
	PDB	3		1sxl	2sxl	2u2f	3sx[1b7£	lovj
	SEO	ğ		88 88 89	1888	1888	1888		6881	1889

PDB annotation	GENE REGULATION/RNA POLY(A) BINDING PROTEIN I, PABP I; RRM, PROTEIN-RNA COMPLEX, GENE REGULATION/RNA	RNA BINDING PROTEIN RNA: BINDING DOMAIN	STRUCTURAL PROTEIN PROTEIN C23; RNP, RBD, RRM, RNA BINDING DOMAIN, NUCLEOLUS	OUTER MEMBRANE PROTEIN OSMOPORIN; OUTER MEMBRANE	PROTEIN, NON-SPECIFIC PORIN, OSMOPORIN, 2 BETA-BARREL, TRANSMEMBRANE		HYDROLASE DOUBLE BETA BARREL, BACTERIAL SERINE PROTEASE		RNA-BINDING DOMAIN RNA- BINDING DOMAIN, ALTERNATIVE SPLICING	RNA-BINDING PROTEIN SPLICING, U2 SNRNP, RBD, RNA-BINDING
Coumpound	POLYDENYLATE BINDING PROTEIN 1; CHAIN: A, B, C, D, E, F, G, H; RNA (5'- R(*AP*AP*AP*AP*AP*AP* AP*AP*AP*AP; CHAIN: M, N, O, P, Q, R, S, T;	HU ANTIGEN C; CHAIN: A;	NUCLEOLIN RBD2; CHAIN: A;	OMPK36; CHAIN: A, B, C;		OUTER MEMBRANE PROTEIN PHOSPHOPORIN (PHOE) IPHO 3	ALPHA-LYTIC PROTEASE; CHAIN: A;	RNA-BINDING PROTEIN SEX- LETHAL PROTEIN (C- TERMINUS, OR SECOND RNA- BINDING DOMAIN 1SXL 3 (RBD-2), RESIDUES 199 - 294 PLUS N-TERMINAL MET) 1SXL 4 (NMR, 17 STRUCTURES) 1SXL 5	SEX-LETHAL PROTEIN; CHAIN: NULL;	SPLICING FACTOR U2AF 65 KD SUBUNIT; CHAIN: A;
SEQFOL D score			r.,		* 1					
PMF score	0.89	1.00	0.65	-0.20		-0.19	-0.19	ે. ક	1.00	0.99
Verify	0.41	0.45	0.42	0.70		0.77	0.89	0.07	0.47	0.44
Psi Blast	3e-05	4.5e-05	3e-05	4.5e-09		7.5e-10	4.5e-08	0.00015	0.00015	1.3e-05
END AA	1313	1313	1320	207		218	204	1299	1313	1313
STAR T AA	1243	1245	1234	14		11	37	1228	1242	1245
CHAI N ID	æ	A	A	¥			Ą	erwie Open	•	Ą
PDB ID	levj	1482	1fjc	losm		1pho	1994	1sxl	2sxl	2u2f
SEQ No.	1889	1889	1889	1889		1889	1889	1889	1889	1889

PDB annotation	PROTEIN	RNA BINDING DOMAIN RNA BINDING DOMAIN, RBD, RNA RECOGNITION MOTIF, RRM, 2 SPLICING INHIBITOR, TRANSLATIONAL INHIBITOR, SEX 3 DETERMINATION, X CHROMOSOME DOSAGE COMPENSATION	RECEPTOR RECEPTOR, SIGNAL TRANSDUCER OF IL-6 TYPE CYTOKINES, THIRD 2 N-TERMINAL DOMAIN, TRANSMEMBRANE, GLYCOPROTEIN	CONNECTIN A71, CONNECTIN; TITIN, CONNECTIN, FIBRONECTIN TYPE III	CONNECTIN A 71, CONNECTING TITIN, CONNECTIN, FIBRONECTIN TYPE III		HEPARIN AND INTEGRIN BINDING HEPARIN AND INTEGRIN BINDING	STRUCTURAL PROTEIN INTEGRIN, HEMIDESMOSOME, FIBRONECTIN, CARCINOMA, STRUCTURAL 2
Coumpound		SEX-LETHAL; CHAIN: A, B, C,	GP130; CHAIN: NULL;	TITIN; CHAIN: NULL;	TITIN; CHAIN: NULL;	NEURAL ADHESION MOLECULE DROSOPHILA NEUROGLIAN (CHYMOTRYPTIC FRAGMENT CONTAINING THE ICFB 3 TWO AMINO PROXIMAL FIBRONECTIN TYPE III REPEATS ICFB 4 (RESIDUES 610 - 814)) ICFB 5	FIBRONECTIN; CHAIN: A;	INTEGRIN BETA-4 SUBUNIT; CHAIN: A, B;
SEQFOL D score						·	57.74	
PMF score		0.55	0.23	0.70	0.94	-0.18		-0.06
Verify		10.0	0.21	0.07	0.18	0.02		0.28
Psi Blast		6e-0 <i>5</i>	1.6e-12	9.6e-11	1.2e-12	1.6e-16	6.4e-28	9.6e-17
END		1335	262	265	266	355	450	348
STAR T AA		1242	166	165	165	162	168	168
CHAI N ID		∢			•		4	٠ \
PDB ID		3sxl	1bj8	1bpv	1bpv	1cfb	ifnh	1983
SEQ NO:		1889	1894	1894	1894	1894	1894	1894

PDB annotation	PROTEIN	STRUCTURAL PROTEIN TENASCIN, FIBRONECTIN TYPE-III, HEPARIN, EXTRACELLULAR 2 MATRIX, ADHESION, FUSION PROTEIN, STRUCTURAL PROTEIN	STRUCTURAL PROTEIN TENASCIN, FIBRONECTIN TURE CHEPARIN, EXTRACELLULAR 2 MATRIX, ADHESION, FUSION PROTEIN, STRUCTURAL PROTEIN	STRUCTURAL PROTEIN TENASCIN, FIBRONECTIN TYPE-III, HEPARIN, EXTRACELLULAR 2 MATRIX, ADHESION, FUSION PROTEIN, STRUCTURAL PROTEIN		RNA BINDING PROTEINRNA XLRBPA; PROTEIN-RNA COMPLEX, DOUBLE STRANDED RNA, PROTEIN-RNA 2 INTERACTIONS, RNA-BINING PROTEIN, RNA BINDING PROTEIN/RNA	SH3 PROTOTYPE WWPROTOTYPE, PROTEIN DESIGN	CELL CYCLE/RNA DSRBDIII; NMR STRUCTURE, PROTEIN/RNA, PROTEIN DSRBD, DROSOPHILA, RNA 2 HAIRPIN	ISOMERASE PIN1; PEPTIDYL-
Coumpound		TENASCIN; CHAIN: A, B;	TENASCIN; CHAIN: A, B;	TENASCIN; CHAIN: A, B;	GLYCOPROTEIN FIBRONECTIN (TENTH TYPE III MODULE) (NMR, 36 STRUCTURES) 1TTF 3	DOUBLE STRANDED RNA BINDING PROTEIN A; CHAIN: A, B; RNA (5- R(*GP*GP*CP*GP*CP*G P*CP*C)-3'); CHAIN: C, D, E, G;	WWPROTOTYPE; CHAIN: A;	MATERNAL EFFECT PROTEIN (STAUFEN); CHAIN: A; STAUFEN DOUBLE-STRANDED RNA BINDING DOMAIN; CHAIN: B;	PEPTIDYL-PROLYL CIS-TRANS
SEQFOL D score						104 mm			
PMF score		0.29	0.12	-0.20	0.49	0.42	0.41	0.70	0.29
Verify score		-0.24	0.09	0.03	0.15	0.30	-0.10	0.57	-0.46
Psi Blast		4.5e-13	9.6e-15	4.8e-15	3e-13	1.1e-07	0.0003	66-12	9000.0
END AA		261	349	450	265	293	49	293	49
STAR T AA		164	169	271	164	230	20	226	11
CHAI		¥	• •	¥			Ą	¥	В
PDB ID		lqr4	lgr4	1qr4	III.	1412	1e0m	Zyeı	1f8a
SEQ NO:		1894	1894	1894	1894	1895	1895	1895	1895

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PDB apposation	PROLINE ISOMERASE, WW DOMAIN, PHOSPHOSERINE BINDING	DOUBLE STRANDED RNA BINDING DOMAIN STAUFEN 1STU 13	
Coumpound	ISOMERASE NIMA- CHAIN: B; Y(SEP)PT(SEP)S PEPTIDE; CHAIN: C;	MATERNAL EFFECT PROTEIN STAUFEN; 1STU 4	
PMF SEQFOL score			
PMF score		0.25	
Verify score		0.18	
Psi Blast		3e-05	
END AA		293	
CHAI STAR NID TAA		233	
CHAI N ID	•		
PDB ID		lstu	
SEQ ID NO:		1895 1stu	

TABLE 6

SEQ ID NO:	Position of Signal in Amino Acid SEquence	maxS (Maximum score)	meanS (Mean score)
949	24	0.926	0.738
950	24	0.976	0.913
951	22	0.982	0.872
952	41	0.937	0.604
953	23	0.896	0.747
954	16	0.945	0.737
955	45	0.964	0.657
956	48	0.994	0.855
957	31	0.984	0.921
958	23	0.966	0.812
959	36	0.994	0.757
960	20	0.977	0.902
961	18	0.968	0.799
962	24	0.882	0.599
963	34	0.921	0.652
964	25	0.921	0.787
965	33	0.967	0.803
966	30	0.978	0.786
967	28	0.980	0.893
968	24	0.976	0.913
969	22	0.984	0.928
970	26	0.949	0.664
971	23	0.996	0.936
972	28	0.929	0.700
973	26	0.976	0.875
974	17	0.919	0.828
975	28	0.976	0.653
976	30	0.996	0.894
977	17	0.953	0.784
978	22	0.982	0.872
979	19	0.890	0.552
980	18	0.984	0.958
981	19	0.981	0.916
982	19	0.995	0.971
983	21	0.980	0.904
984	21	0.980	0.904
985	16	0.961	0.916
986	26	0.951	0.801
987	43	0.992	0.943
988	41	0.937	0.604
989	43	0.994	0.659
990	29	0.986	0.848
991	37	0.984	0.878
992	19	0.942	0.693
993	22	0.982	0.872
995	19	0.982	0.931
996	22	0.993	0.807
997	28	0.992	
998	23		0.919
		0.896	0.747
999	23	0.985	0.951
1000	21	0.989	0.925
1001	11	0.900	0.758
1002	18	0.933	0.634
1004	16	0.881	0.607

SEQ ID NO:	Position of Signal in Amino Acid SEquence	maxS (Maximum score)	meanS (Mean score)
1005	18	0.964	0.812
1006	19	0.972	0.915
1007	24	0.997	0.929
1008	16	0.945	0.737
1009	31	0.957	0.775
1010	22	0.975	0.822
1011	28	0.946	0.799
1012	24	0.973	0.910
1013	29	0.968	0.769
1014	25	0.977	0.776
1015	41	0.986	0.847
1016	28	0.988	0.938
1017	23	0.976	0.897
1018	45	0.964	0.657
1019	28	0.956	0.604
1020	33	0.948	0.776
1021	18	0.930	0.679
1022	26	0.947	0.594
1023	31	0.991	0.925
1024	41	0.942	0.703
1025	36	0.910	0.749
1026	24	0.988	0.919
1027	27	0.962	0.696
1028	23	0.965	0.693
1029	22	0.962	0.919
1030	24	0.943	0.832
1031	34	0.973	0.817
1032	22	0.947	0.677
1033	25	0.889	0.718
1034	27	0.962	0.856
1035	19	0.967	0.909
1036	39	0.986	0.922
1037	28	0.982	0.924
1038	44	0.974	0.662
1039	29	0.984	0.763
1040	22	0.974	0.796
1041	29	0.928	0.725
1051	23	0.966	0.812
1054	19	0.951	0.895
1055	16	0.927	0.827
1056	25	0.949	0.823
1058	28	0.980	0.848
1061	24	0.965	0.891
1062	25	0.946	1:- 5:2
1067	36	0.964	0.860
1074	32		0.648
1076	17	0.941	0.669
		0.995	0.974
1083	18	0.968	0.799
1089	24	0.882	0.599
1091	38	0.991	0.904
1094	29	0.963	0.888
1096	19	0.892	0.715
1101	34	0.921	0.652
1102	20	0.951	0.839
1106	31	0.921	0.659
1110	36	0.992	0.917

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SEQ ID NO:	Position of Signal in Amino Acid SEquence	maxS (Maximum score)	meanS (Mean score)
1124	30	0.989	0.910
1125	28	0.974	0.851
1127	25	0.937	0.812
1130	30	0.978	0.786
1131	27	0.987	0.879
1133	23	0.923	0.655
1144	28	0.980	0.893
1147	27	0.963	0.833
1150	24	0.976	0.913
1151	24	0.988	0.967
1152	22	0.968	0.831
1154	21	0.952	0.822
1155	42	0.939	0.682
1157	22	0.984	0.928
1158	22	0.984	0.928
1165	21	0.942	0.713
1167	18	0.922	0.838
1170	18	0.988	0.944
1170	18		0.958
1174		0.975	
1173	18	0.975	0.958
1176	18	0.975	0.958
1177	48	0.989	0.889
1178	23	0.996	0.936
1180	16	0.967	0.933
1193	15	0.948	0.907
1195	27	0.936	0.689
1196	42	0.978	0.750
1197 ·	15	0.977	0.966
1199	26	0.976	0.875
1200	28	0.973	0.822
1201	28	0.990	0.925
1205	22	0.982	0.933
1206	15	0.986	0.919
1207	27	0.994	0.900
1215	21	0.989	0.871
1220	28	0.976	0.653
1226	20	0.987	0.916
1229	30	0.996	0.894
1230	41	0.983	0.791
1234	20	0.978	0.893
1239	17	0.953	0.784
1240	25	0.950	0.897
1241	20	0.974	
1242			0.912
	15	0.974	0.817
1247	35	0.973	0.795
1250	22	0.982	0.872
1251	18	0.983	0.927
1254	20	0.934	0.828
1255	16	0.952	0.807
1256	19	0.904	0.656
1260	35	0.957	0.640
1261	35	0.957	0.640
1263	33	0.953	0.707
1264	24	0.981	0.884
1265	24	0.987	0.914
1266	21	0.977	0.905
1200	+1	U.211	0.200

SEQ ID NO:	Position of Signal in Amino Acid SEquence	maxS (Maximum score)	meanS (Mean score)
1267	24	0.978	0.911
1268	18	0.984	0.958
1269	18	0.984	0.958
1270	24	0.989	0.922
1271	18	0.984	0.956
1272	18	0.986	0.965
1273	18	0.986	0.965
1276	32	0.956	0.706
1277	48	0.983	0.616
1278	20	0.965	0.878
1282	16	0.921	0.828
1283	20	0.937	0.700
1293	19	0.995	0.971
1294	19	0.995	0.971
1296	20	0.926	0.751
1302	29	0.981	0.937
1310	27	0.977	0.849
1314	24	0.977	0.845
1315	23	0.990	0.833
1317	25	0.971	0.894
1318	16	0.961	0.916
1319	41	0.980	0.681
1328	17	0.977	0.921
1329	26	0.993	0.894
1331	25	0.986	0.939
1333	33	0.977	0.811
1340	43	0.992	0.943
1341	20	0.943	0.882
1343	20	0.995	0.933
1344	26	0.938	0.663
1346	21	0.955	0.767
1347	19	0.920	0.692
1348	41	0.937	0.604
1349	41	0.937	0.604
1353	19	0.986	0.961
1357	41	0.923	0.559
1359	25	0.973	0.853
1361	20	0.935	0.817
1364	29	0.958	0.637
1365	23	0.991	0.740
1368	29	0.986	0.848
1369	18	0.997	0.979
1373	16	0.979	0.979
1375	25		
1376	37	0.980	0.952
1378	37	0.989	0.822
1379		0.984	0.878
	42	0.978	0.698
1380	18	0.969	0.913
1383	31	0.981	0.856
1386	36	0.987	0.595
1387	27	0.955	0.786
1389	17	0.915	0.825
1390	34	0.954	0.783
1393	19	0.941	0.839
1396	27	0.944	0.778
1397	20	0.941	0.734

SEQ ID NO:	Position of Signal in Amino Acid SEquence	maxS (Maximum score)	meanS (Mean score)
1404	22	0.982	0.872
1427	19	0.993	0.931
1428	22	0.992	0.807
1430	22	0.918	0.716
1433	38	0.994	0.887
1436	24	0.914	0.588
1438	28	0.990	0.919
1442	26	0.990	0.969
1446	36	0.954	0.817
1450	23	0.896	0.747
1451	23	0.969	0.855
1456	24	0.985	0.932
1462	23	0.985	0.951
1464	27	0.985	0.927
1465	21	0.960	0.740
1467	41	0.990	0.922
1468	20	0.991	D 054
1469	20	0.991	0.954
1473	21	0.975	0.909
1478	11	0.900	
1493	18	0.933	0.758
1495	22		0.634
1496	40	0.899	0.639
		0.953	0.668
1509	16	0.881	
1516	36	0.924	0.590
1517	25	0.919	0.718
1518	28	0.928	0.590
1519	27	0.967	0.872
1526	25	0.998	0.934
1527	30	0.973	0.829
1547	20	0.937	0.728
1551	30	0.962	0.801
1552	17	0.925	0.779
1557	20	0.981	0.910
1562	17	0.977	0.921
1565	25	0.938	0.677
1568	22	0.975	0.822
1577	34	0.934	0.552
1578	2.8	0.946	0.799
1583	15	0.954	0.725
1584	30	0.938	0.808
1592	24	0.973	0.910
1597	24	0.920	0.596
1600	29	0.968	0.769
1604	28	0.975	0.926
1613	25	0.977	0.776
1618	41		
1627	24	0.986	0.847
1630		0.915	0.578
	24	0.950	0.737
1631	28	0.987	0.785
1632	19	0.890	0.552
1633	22	0.968	0.934
1634	22	0.968	0.934
1635	23	0.965	0.883
1636	23	0.965	0.883
1638	26	0.896	0.615



SEQ ID NO:	Position of Signal in Amino Acid SEquence	maxS (Maximum score)	meanS (Mean score)
1641	30	0.956	0.665
1644	39	0.971	0.694
1646	44	0.992	0.576
1649	45	0.964	0.657
1650	45	0.964	0.657
1653	17	0.968	0.947
1655	28	0.960	0.607
1657	31	0.977	0.720
1662	28	0.956	0.604
1666	47	0.985	0.646
1667	19	0.990	0.946
1677	47	0.996	0.556
1684	18	0.930	0.679
1687	25	0.992	0.948
1689	26	0.947	0.594
1693	22	0.963	0.859
1695	26	0.956	0.830
1703	26	0.990	0.959
1706	40	0.987	0.917
1707	26	0.985	0.917
1710	36	0.991	0.868
1713	24	0.887	0.553
1714	23	0.995	0.974
1715	18	0.997	0.977
1716	22	0.968	0.934
1718	26	0.974	0.730
1721	18	0.983	0.939
1731	24	0.988	0.919
1743	30	0.939	0.639
1744	26	0.984	0.746
1755	23	0.965	0.693
1758	22	0.962	0.919
1759	21	0.988	0.911
1760	36	0.980	0.559
1769	10	0.880	0.780
1771	14	0.922	0.678
1773	39	0.982	0.829
1778	34	0.973	0.817
1779	36	0.976	0.794
1786	18	0.918	0.651
1787	35	0.991	0.834
1789	22	0.947	0.677
1795	24	0.963	0.865
1796	30	0.967	0.758
1797	33	0.926	0.807
1800	25	0.889	0.718
1805	20	0.995	0.968
1807	27	0.887	0.642
1810	41	0.975	0.875
1813	26	0.921	0.620
	36	0.951	0.782
1826		0.983	0.888
1832	19	0.983	0.941
1833	23	The second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second secon	
1834	40	0.964	0.560
1839	39	0.942	0.587
1846	16	0.945	0.737

SEQ ID NO:	Position of Signal in Amino Acid SEquence	max\$ (Maximum score)	meanS (Mean score)
1847	24	0.946	0.593
1848	14	0.974	0.662
1850	26	0.974	0.730
1851	2.7	0.952	0.832
1856	25	0.960	0.642
1866	31	0.956	0.846
1869	16	0.968	0.921
1884	19	0.984	0.936

TABLE 7

SEQ ID	Chromsomal location
1 .	X
2	Xp21.2-p11.2
3	2
4	2
5	8
6	8
7	17
10	17
13	9
14	Xq24-q25
15	Xq24-q25
16	9p21
17	16
19	7q32
20	2
21 18 16 17 18 18 18 18 18 18 18 18 18 18 18 18 18	2
22	11
23	12q
27	22q11
28	6p
29	6p23
31 (100) 100 (100) 100 (100)	17q
32	12
33	2p23.3-q34
34	9q31-q32
35	19
36	19
37	19q13.3
38	6p21.3
39	10g26.2-10g26.3
40	3
42	12
43	6p21-p12
44	13q12-13
46	2
47 - 12/4/2011 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	3
48	15q15
49	22q13.33
50	5q14-q22
51	X
52.	19cen-q13.2
53	3p26

SEQ ID_	Chromsomal location
54	2p24.3
55	3p26
56	3p26
57	15
60	15
62	1p21.2-22.3
65	11q12-q13.1
66	xpi1
67	20q11.21-q13.12
69	2 X
70 71	1
72	1q21,2-q21.3
73	17p11.2
74	X
75	19
76	9
80	19
83	6q16
85	15
86	12
87	17q22-q24
88	8q22-q23
90	15
91	14932.3
94	14
95 96	7
96 97	10q26.1 9p21
98	16924.3
99	5
101	15
102	19
103	6p21.3
104	11p15.3-p15.4
105	16
107	14q32.1-q32.2
111	11q13
112	9
114	2935
115	22q13
116	16 16
117 118	16924.3
120	19
122	
123	20
124	9
125	3
126	11
127	22911.2
128	20q11,2-12
129	14
131	10q25.1
133	17p11.2
134	20
136	4p16.3

SEQ ID	Chromsomal location
137	12p13
138	19
139	1p34.1-p32
140	4 or 17
143	Xq13.1-13.3
144	3
145	3
146	5
147	9
148	11q13
149	6
150	15
151	19
152	Xp11.21-11.23
153	18q22-q23
155	16
157	4
160	1p36.23-p33
161	9q22.2
163	4
165	3
166	17
167	6p21.3
168	16
169	9
170	19
171	15
172	2p25
173	22q11.21
174	18q22
179	бр21.3
180	15q14
181	5q
183	5
184	11
187	11
188	3p21.3
189	12p13-qter
190	12p13-qter
191	12p13-qter
192	12p13-qter
193	2q34-q35
194	2q34-q35
195	10
199	7911-922
200	7q22.1-7q31.33
201	3
202	19q13.4
203	3
205	Xq28
206	6
208	Xq26.2-27.2
209	4
210	4
211	1q31
212	19q12-19q13.1
213	6q23
07	

SEQ ID	Chromsomal location
214	10
215	
216	1p32.2-34.2
217	8
218	11q13
219	1q21-q23
220	Xq28
221	16
222 223	1
224	19p13.3
225	19p11-q11
226	1
227	1
228	1
229	12
230	5
231	1p31
232	1p31.1-p22.3
233	22q11.23
234	22q12.1-q12.3
235	
236	17
237	15
238	2p13 17
239	
241	11p13
242 243	4q22-q24
244	12
245	19
246	5
247	14
248	16
249	14
250	4
251	19
252	9p22-p21_or_9p13
256	119
257	9q33-q34.1
258	12pter-p13.31
260	8
261	11q14
262	17
263	12q13 16q13-q21
264	16q13-q21
265 267	6q26-27
268	9q12-q21.2
269	9q12-q21.2
	9q12-q21.2
	1 901 2-021.2
270	
270 271	19
270 271 272	19 1p34.1-35.3
270 271 272 273	19 1p34.1-35.3 11
270 271 272 273 274	19 1p34.1-35.3
270 271 272 273	19 1p34.1-35.3 11



SEQ ID	Chromsomal location
278	16
280	19q13.1-q13.2
282	12
284	2p23.3-q24.3
285	11p15
286	19
287	7
288	10
290	12
293	3q23-q24
294	1p34.1-35.3
295	p22.2-31.1
296	3q22-q24
297	6
299 300	2p11 16
301	10q24
302	10
304	12q22-q23
305	17pter-p11
307	1p35-p34
308	9
309	16
310	21
311	12p13
312	1
313	
314	17
315	1q42-q43
316	6p21.32-22.1
317	6p21.32-22.1
318	6p21.32-22.1
319	6p21.32-22.1
320 321	6p21.32-22.1 6p21.32-22.1
322	6p21.32-22.1
323	6p21.32-22.1
324	6p21.32-22.1
325	6p21.32-22.1
326	17
327	3
328	14
332	17
335	17
336	14q32
337	8q23
338	8q23
339	16q11.1-q11.2
340	8q22-q23
341	16p13.3
342	18
343	15
344	17
345	20q11.2-q13.1
346	20q11.2-q13.1
347	19q13.3
348	19

	SEQ ID	Chromsomal location
	349	17q25.1
	350	18
	351	11
A	352	1
	353	q25.1-31.1
Ď	354	11q14
	355	1q31
	356	1q31
-	357	18
	358	3p
	359	10
•	360	7q22
	361	7q22
	362	1q21.3
	363	3
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	367	14
•	369	1p36.21
	371	6p12.3-21.1
	373	14q13.1-14q21.3
	374	15
	375	4
	376	7q32-q34
	377	7q32-q34
entre de la companya de la companya de la companya de la companya de la companya de la companya de la companya	378	20q13.1-q13.2
	381	13
	382	1q21.2-22
		16
最高的 ,特别 的特别的特别。	384 385	12 20q13.1
and the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of t	386	16
	387	8q21.3-q22.1
필요 (1985년 - 1915년 - 1914년 - 1	388	11
	389	15q22.1
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	394	8q23
	395	15q24-q26
Andrew Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the	396	15922
	397	7q34-q36
	399	2
	400	6q21-22
	401	6q21-22
	402	14q24.3
	403	2
	404	11q13
	405	17
	407	14
	408	10
en 🍁 vere verker beskriften.	409	10q23-q24
	410	19
	411	11
	412	11p15
,	413	12q13.2-q13.3
	414	3p13-q26.1
·	416	17
I		

SEQ ID	Chromsomal location
421	5q35
422	3
423	12
424	3p24.3
425	19
426	6p21.1-21.2
427	6
428	22q13,2-q13.31
429	11
430	2
432	14q31
433	17
434	22
436	7q35
440	8p11.2
441	11q12
443	5
444	
445	13q13
446	17
447	17
448	lp35.2-36.13
449	6
450	15q24-q25
451	19
452	4
453	2
454	11
455	17 (4.8 14.4 6)
456	10
457	p31.3-32.2
458	1
459	7p13-p11.2
460	12
461	18p11.2
462	17
463	22q11.2
464	16
466	17
467	11q23
468	3
469	7q32
470	1
472	19
473	19
474	p33-34.3
475	7q36
476	2
477	9p24.1-24.3
478	6p22.1-22.3
479	20
480	22q12.3-13.1
480 481	22q12.3-13.1 16q22.1-q22.3
480	22q12.3-13.1 16q22.1-q22.3 19
480 481	16q22.1-q22.3
480 481 483 484	16q22.1-q22.3 19
480 481 483	16q22.1-q22.3 19 19

SEQ ID	Chromsomal location	
492	4926-927	
493	2p13	
494	Ø	
495		
496		
497	7 q23.2-q25.3	
498	Ilq	
499	4p15.31	
500	10	
501	8q24.3	
503	18	
504	2	
505	19	
506		
507	3p14.3	
	14	
508	11p15.5	
509	11	
510	15q25	
511	14q21.1-q22.3	
512	13q11	
513	10	
514	Xq28	
515	15q15	
516	19p13.3	
518	14q21	
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519	13	
520	12	
521	12	
522	20q12-q13.12	
523	6q22.1-22.33	
524	12	
526	16	
527	17	
528	3	
529	6p21.3	
530	1q42.13-43	
531	16p	
532	17	
533	16q24.1	
534	19p13.3-p13.2	
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770	14
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784	8p11.2
785	8 12.100 (2.10) (2.10)
786	8
787	17
788	8
789	1942.13-43
790	7q11.21-q11.23
791	11
792	3p13-q13.2
793	9
794	11q12
795	1p32.2-34.2
797	18
798	18
799	11q13
800	17
801	7p15-p21
802	17
803	17p13.1
805	17q25.3
806	17q25
808	5
809	7p15-p14
810	9q34.2-q34.3
811	1
812	6
813	8
814 815	17 20

SEQ ID	Chromsomal location
816	7q34-q36
817	14q21.1-q21.3
818	1p32.1-33
819	5
820	6p21.3
821	17
822	15
823	5
824	19
825 826	1p32.3
826	11
828	p34.1-34.3
829	16
830	8p11.2
831	17q21.3-17q22
833	17
834	7p
835	21
836	10cen-q26.11
837	19
838	5
840	10
841	7q11-q22
842	11
843	17
844	3
845	17
846	17
847 848	17
849	10
850	5q
851	5
853	7q35-qter
854	19
855	19
857	8
858	16
860	10
861	19
863	18p11.2
864	17
866	15q15
867	7
868	12
869	1
870	11q23
871	16
872	16p13.3
873	17q12-q21
874	11q13.5
875 876	11cen-q12.1
877	16q13
878	X 1021 222
879	1q21-q23
0/3	xq22.1-q22.3

SEQ ID	Chromsomal location
880	1p31.2-32.3
881	19q13.3-q13.4
883	3p
884	7
885	14q32
886	2
887	22q11.2
888	12
889	15
890	18
891	17
892	Xq21.33-22.3
893	6p21.32-22.2
894	111
895	7q33-q34
897	13
898	15
901	1
902	14
904	16p11.2
905	21q22.3
907	10
909	X
910	10q26
911	20
912	1
913	18
914	6
915	10
916	13
917	17
919	15q15
920	20
921	22q12.3
922	16
923	11
924	2q33.3
927	9
928	2q21
929	19
930	18
931	16
932	16
934	11p15
936	7935
937	6922.1-22.33
939	17
940	17
941	17
942	4
943	1p36.31-p36.11
944	9
944	12
946	19p13.3
947	22q11.2
948	5

TABLE 8

SEQ ID No of Full-length Nucleotide Sequence	SEQ ID NO of Full-length Peptide Sequence	SEQ ID NO in Priority Application USSN 09/799,451
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6	954	6
7	955	7
8	956	8
9	957	9
10	958	10
11	959	11
12	960	12
13	961	13
14	962	14
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16	964	16
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18	966	18
19	967	19
20	968	20
21	969	21
22	970	22
23	971	23
24	972	24
25	973	25
26	974	26
27	975	27
28	976	28
29	977	29
30	978	30
31	979	31
32	980	32
33	981	33
34	982	34
35	983	35
36	984	36
37	985	37
38	986	38
39	987	39
40	988	40
41	989	41
42	990	42
43	991	43
44	992	44
45	993	45
46	994	46
47	995	47
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49	997	49
	998	50
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51	999	52
52	1000	53
53	1001	
54	1002	54

SEQ ID NO of Full-length Nucleotide Sequence	SEQ ID NO of Full-length	SEQ ID NO in Priority Application USSN 09/799,451
55	Peptide Sequence	55 USSIN 09/799,431
56	1004	56
57	1005	57
58	1006	58
59	1007	59
60	1008	60
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62	1010	61 62
63	1011	63
64	1012	64
65	1013	65
66	1014	66
67	1015	67
68	1016	68
	1017	
69	1018	69 70
70		
72	1019 1020	71 72
73	1021	73 74
	1022	
75	1023	75
76	1024	76
77	1025	77
78	1026	78
79	1027	79
80	1028	80
81	1029	81
82	1030	82
83	1031	83
84	1032	84
85	1033	85
86	1034	86
87	1035	87
88	1036	00
89	1037	89
90	1038	90
91	1039	91
92	1040	92
93	1041	93
94	1042	94
95	1043	95
96	1044	96
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98	1046	98
99	1047	99
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102	1050	102
103	1051	103
104	1052	104
105	1053	105
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108	1056	108
109	1057	109
110	1058	110

SEQ ID NO of Full-length Nucleotide Sequence	SEQ ID NO of Full-length Peptide Sequence	SEQ ID NO in Priority Applica USSN 09/799,451
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113	1061	113
114	1062	114
115	1063	115
116	1064	116
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119	1067	119
120	1068	120
121	1069	121
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124	1072	124
125	1073	125
126	1074	126
127	1075	127
128	1076	128
129	1077	129
130	1078	130
131	1079	131
132	1080	132
133	1081	133
134	1082	134
135	1083	135
136	1084	136
137	1085	137
	1006	138 0.81000 4
138	1087	
139		139
140	1088	140
141	1089	141
142	1090	142
143	1091	143
144	1092	144
145	1093	145
146	1094	146
147	1095	147
148	1096	148
149	1097	149
150	1098	150
151	1099	151
152	1100	152
153	1101	153
154	1102	154
		155
155	1103	
156	1104	156
157	1105	157
158	1106	158
159	1107	159
160	1108	160
161	1109	161
162	1110	162
163	1111	163
164	1112	164
165	1113	165

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SEQ ID NO of Full-length Nucleotide Sequence	SEQ ID NO of Full-length Peptide Sequence	SEQ ID NO in Priority Application USSN 09/799,451
167	1115	167
168	1116	168
169	1117	169
170	1118	170
171	1119	171
172	1120	172
173	1121	173
174	1122	174
175	1123	175
176 177	1124	176
	1125	177
178 179	1126	178
180	1127	179
181	1128	180
182	1129	181
183	1130	182
184	1131	183
185	1132	184
186	1133	185
187	1134	186
188	1135 1136	187
189	1137	188
190	1138	189
191	1139	190
192	1140	191
193	1141	192
194	1142	193 194
195	1143	
196	1144	195 196
197	1145	190
198	1146	198
199	1147	199
200	1148	200
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202	1150	202
203	1151	203
204	1152	204
205	1153	205
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207	1155	207
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209	1157	209
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SEQ ID NO of Full-length Nucleotide Sequence	SEQ ID NO of Full-length Peptide Sequence	SEQ ID NO in Priority Application USSN 09/799,451
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228	1176	228
229	1177	229
230	1178	230
231	1179	231
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233	1181	233
234	1182	234
235	1183	235
236	1184	236
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238	1186	238
239	1187	239
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252	1200	252
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254	1202	254
255 256	1203	255
257	1204 1205	256 257
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259	1207	259
260	1208	259
261	1209	261
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263	1211	263
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272	1220	272
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	006	1-17

SEQ ID NO of Full-length Nucleotide Sequence	SEQ ID NO of Full-length Peptide Sequence	SEQ ID NO in Priority Application USSN 09/799,451
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293	1241	293
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322	1270	322
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326	1274	326
327	1275	327
328	1276	328
329	1277	329
330	1278	330
331	1279	331
332	1280	332
333	1281	333
334	1282	334

SEQ ID NO of Full-length Nucleotide Sequence	SEQ ID NO of Full-length Peptide Sequence	SEQ ID NO in Priority Application USSN 09/799,451
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336	1284	336
337	1285	337
338	1286	338
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352	1300	352
353	1301	353
354	1302	354
355	1303	355
356	1304	356
357	1305	357
358	1306	358
359	1007	359
360	1308	360
361	1309	361
362	1310	362
363	1311	363
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364 365	1313	365
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371	1319 1320	372
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390	1338	390



SEQ ID NO of Full-length Nucleotide Sequence	SEQ ID NO of Full-length Peptide Sequence	SEQ ID NO in Priority Application USSN 09/799,451
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422	1370	422
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SEQ ID NO of Full-length Nucleotide Sequence	SEQ ID NO of Full-length Peptide Sequence	SEQ ID NO in Priority Application US\$N 09/799,451
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456	1404	456 457
457	1405	458
458	1406	459
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463	1411	463
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487 488	1435 1436	488
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SEQ ID NO of Full-length Nucleotide Sequence	SEQ ID NO of Full-length Peptide Sequence	SEQ ID NO in Priority Application USSN 09/799,451
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SEQ ID NO of Full-length Nucleotide Sequence	SEQ ID NO of Full-length Peptide Sequence	SEQ ID NO in Priority Application USSN 09/799,451
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SEQ ID NO of Full-length Nucleotide Sequence	SEQ ID NO of Full-length Peptide Sequence	SEQ ID NO in Priority Application USSN 09/799,451
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623	1571	623
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628	1576	628
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630	1578	630
631	1579	631
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633	1581	633
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659	1607	
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661	1609	661
662	1610	662
663	1611	663
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SEQ ID NO of Full-length Nucleotide Sequence	SEQ ID NO of Full-length Peptide Sequence	SEQ ID NO in Priority Application USSN 09/799,451
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708	1656	707
709	1657	708
710	1658	709
711	1659	710
712		711
	1660	712
713	1661	713
714	1662	714
715	1663	715
716	1664	716
717	1665	717
718	1666	718
719	1667	719
720	1668	720
721	1669	721
722	1670	722
723	1671_	723
724	1672	724
725	1673	725
726	1674	726

SEQ ID NO of Full-length Nucleotide Sequence	SEQ ID NO of Full-length Peptide Sequence	SEQ ID NO in Priority Application USSN 09/799451
727	1675	727
728	1676	728
729	1677	729
730	1678	730
731	1679	731
732	1680	732
733	1681	733
734	1682	734
735	1683	735
736	1684	736
737	1685	737
738	1686	738
739	1687	739
740	1688	740
741	1689	741
742	1690	742
743	1691	743
744	1692	744
745	1693	745
746	1694	746
747	1695	747
748	1696	748
749	1697	749
750	1698	750
751	1699	751
752	1700	752
753	1701	753
754	1702	754
755	1703	755
756	1704	756
757	1705	757
758	1706	758
759	1707	759
760	1708	760
761	1709	761
762	1710	762
763	1711	763
764	1712	764
765	1713	765
766	1714	766
767	1715	767
768	1716	768
769	1717	769
770	1718	770
771	1719	771
772	1720	772
773	1721	773
774	1722	774
775	1723	775
776	1724	776
777	1725	777
778	1726	778
779	1727	778
780	1728	
781	1729	780
/O1	1147	781

SEQ ID NO of Full-length Nucleotide Sequence	SEQ ID NO of Full-length Peptide Sequence	SEQ ID NO in Priority Application USSN 09/799,451
783	1731	783
784	1732	784
785	1733	785
786	1734	786
787	1735	787
788	1736	788
789	1737	789
790	1738	790
791	1739	791
792 793	1740	192
793	1741	793
794	1742	794
796	1743 1744	795
797		796
798	1745 1746	797 798
799	1747	799
800	1748	800
801	1748	801
802	1750	802
803	1751	803
804	1752	804
805	1753	805
806	1754	806
807	1755	807
808	1756	808
809	1757	809
810	1758	810
811	1759	811
812	1760	812
813	1761	813
814	1762	814
815	1763	815
816	1764	816
817	1765	817
818	1766	818
819	1767	819
820	1768	820
821	1769	821
822	1770	822
823	1771	823
824	1772	824
825	1773	825
826	1774	826
827	1775	827
828	1776	828
829	1777	829
830	1778	830
831	1779	831
832	1780	832
833	1781	833
834	1782	834
835	1783	835
836	1784	836
837	1785	837
838	1786	838

SEQ ID NO of Full-length Nucleotide Sequence	SEQ ID NO of Full-length Peptide Sequence	SEQ ID NO in Priority Application USSN 09/799,451
839	1787	839
840	1788	840
841	1789	841
842	1790	842
843	1791	843
844	1792	844
845	1793	845
846	1794	846
847	1795	847
848	1796	848
849	1797	849
850	1798	850
851	1799	851
852	1800	852
853	1801	853
854	1802	854
855	1803	855
856	1804	856
857	1805	857
858	1806	858
859		859
860	1808	860
861	1809	861
862	1810	862
863	1811	963
864	1812	864
865	1813	865
866	1814	866
867	1815	0.00
868	1816	
869	1817	868 869
870	1818	870
871	1819	871
872	1000	000
873	1821	
874	1822	873
875	1823	874
876		875
877	1824	876
878	1825 1826	877
879		878
880	1827	879
	1828	880
881	1829	881
882	1830	882
883	1831	883
884	1832	884
885	1833	885
886	1834	886
887	1835	887
888	1836	888
889	1837	889
890	1838	890
891	1839	891
892	1840	892
893	1841	893
894	1842	894

SEQ ID NO of Full-length Nucleotide Sequence	SEQ ID NO of Full-length Peptide Sequence	SEQ ID NO in Priority Application USSN 09/799,451
895	1843	895
896	1844	896
897	1845	897
898	1846	898
899	1847	899
900	1848	900
901	1849	901
902	1850	902
903	1851	903
904	1852	904
905	1853	905
906	1854	906
907	1855	907
908	1856	908
909	1857	909
910	1858	910
911	1859	911
912	1860	912
913	1861	913
914	1862	914
915	1863	915
916	1864	916
917	1865	917
918	1866	918
919	1867	919
920	1868	920
921	1869	921
922	1870	922
923	1871	923
924	1872	924
925	1873	925
926	1874	926
927	1875	927
928	1876	928
929	1877	929
930	1878	930
931 932	1879	931
	1880	932
933 934	1881	933
	1882	934
935	1883	935
936	1884	936
937	1885	937
938	1886	938
939	1887	939
940	1888	940
941	1889	941
942	1890	942
943	1891	943
944	1892	944
945	1893	945
946	1894	946
947	1895	947
948	1896	948

CLAIMS

WHAT IS CLAIMED IS:

 An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of SEQ ID NO: 1 – 948, a mature protein coding portion of SEQ ID NO: 1 – 948, an active domain coding protein of SEQ ID NO: 1 – 948, and complementary sequences thereof.

- 2. An isolated polynucleotide encoding a polypeptide with biological activity, wherein said polynucleotide has greater than about 90% sequence identity with the polynucleotide of claim 1.
 - 3. The polynucleotide of claim 1 wherein said polynucleotide is DNA.

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- 4. An isolated polynucleotide of claim 1 wherein said polynucleotide comprises the complementary sequences.
- 5. A vector comprising the polynucleotide of claim 1.

- 6. An expression vector comprising the polynucleotide of claim 1.
- 7. A host cell genetically engineered to comprise the polynucleotide of claim 1.
- 8. A host cell genetically engineered to comprise the polynucleotide of claim 1 operatively associated with a regulatory sequence that modulates expression of the polynucleotide in the host cell.
- 9. An isolated polypeptide, wherein the polypeptide is selected from the group consisting of a polypeptide encoded by any one of the polynucleotides of claim 1 (i.e. SEQ ID NO: 949-1896).
 - 10. A composition comprising the polypeptide of claim 9 and a carrier.

11. An antibody directed against the polypeptide of claim 9.

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- 12. A method for detecting the polynucleotide of claim 1 in a sample, comprising:
- a) contacting the sample with a compound that binds to and forms a complex with the polynucleotide of claim 1 for a period sufficient to form the complex; and
- b) detecting the complex, so that if a complex is detected, the polynucleotide of claim 1 is detected.
- 13. A method for detecting the polynucleotide of claim 1 in a sample, comprising:
- a) contacting the sample under stringent hybridization conditions with nucleic acid primers that annual to the polynucleotide of claim 1 under such conditions;
 - b) amplifying a product comprising at least a portion of the polynucleotide of claim 1; and
 - c) detecting said product and thereby the polynucleotide of claim 1 in the sample.
 - 14. The method of claim 13, wherein the polynucleotide is an RNA molecule and the method further comprises reverse transcribing an annealed RNA molecule into a cDNA polynucleotide.
 - 15. A method for detecting the polypeptide of claim 9 in a sample, comprising:
 - a) contacting the sample with a compound that binds to and forms a complex with the polypeptide under conditions and for a period sufficient to form the complex; and
 - b) detecting formation of the complex, so that if a complex formation is detected, the polypeptide of claim 9 is detected.
 - 16. A method for identifying a compound that binds to the polypeptide of claim 9, comprising:
 - a) contacting the compound with the polypeptide of claim 9 under conditions sufficient to form a polypeptide/compound complex; and
 - b) detecting the complex, so that if the polypeptide/compound complex is detected, a compound that binds to the polypeptide of claim 9 is identified.

17. A method for identifying a compound that binds to the polypeptide of claim 9, comprising:

- a) contacting the compound with the polypeptide of claim 9, in a cell, under conditions sufficient to form a polypeptide/compound complex, wherein the complex drives expression of a reporter gene sequence in the cell; and
- b) detecting the complex by detecting reporter gene sequence expression, so that if the polypeptide/compound complex is detected, a compound that binds to the polypeptide of claim 9 is identified.

18. A method of producing the polypeptide of claim 9, comprising,

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- a) culturing a host cell comprising a polynucleotide sequence selected from the group consisting of a polynucleotide sequence of SEQ ID NO: 1-948, a mature protein coding portion of SEQ ID NO: 1-948, an active domain coding portion of SEQ ID NO: 1-948, complementary sequences thereof, under conditions sufficient to express the polypeptide in said cell; and
 - b) isolating the polypeptide from the cell culture or cells of step (a).
- 19. An isolated polypeptide comprising an amino acid sequence selected from the group consisting of any one of the polypeptides from the Sequence Listing, the mature protein portion thereof, or the active domain thereof.
- 20. The polypeptide of claim 21 wherein the polypeptide is provided on a polypeptide array.
- 21. A collection of polynucleotides, wherein the collection comprising the sequence information of at least one of SEQ ID NO: 1-948.
- 22. The collection of claim 21, wherein the collection is provided on a nucleic acid array.
- 23. The collection of claim 22, wherein the array detects full-matches to any one of the polynucleotides in the collection.

24. The collection of claim 22, wherein the array detects mismatches to any one of the polynucleotides in the collection.

25. The collection of claim 21, wherein the collection is provided in a computer-readable format.

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- 26. A method of treatment comprising administering to a mammalian subject in need thereof a therapeutic amount of a composition comprising a polypeptide of claim 9 or 19 and a pharmaceutically acceptable carrier.
- 27. A method of treatment comprising administering to a mammalian subject in need thereof a therapeutic amount of a composition comprising an antibody that specifically binds to a polypeptide of claim 9 or 19 and a pharmaceutically acceptable carrier.